

1/60

5' 9 18 27 36 45 54
GTG GGC ATG GTG GGC AAC GTC CTG CTG GTG CTG GTG ATC GCG CCG GTG CGC CGG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Gly Met Val Gly Asn Val Leu Leu Val Leu Val Ile Ala Arg Val Arg Arg

 63 72 81 90 99 108
CTG CAC AAC GTG ACG AAC TTC CTC ATC GGC AAC CTG GCC TTG TCC GAC GTG CTC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu

 117 126 135 144 153 162
ATG TGC ACC GCC TGC GTG CCG CTC ACG CTG GCC TAT GCC TTC GAG CCA CGC GGC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Met Cys Thr Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly

 171 180 189 198 207 216
TGG GTG TTC GGC GGC GGC CTG TGC CAC CTG GTC TTC TTC CTG CAG CCG GTC ACC
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr

 225 234 243 252 261 270
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CCG TAC GTC GTG
--- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val

 279 288 297
CTG GTG CAC CCG CTG AGG CCG CGC ATC 3'
--- --- --- --- --- --- --- --- --- ---
Leu Val His Pro Leu Arg Arg Arg Ile

FIG. 1

BEST AVAILABLE COPY

5'	9	18	27	36	45	54
	GGC CTG CTG GTC ACC TAC CTG CTC CCT CTG CTG ATC CTC CTG TCT TAC					
	---	---	---	---	---	---
	Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr					
	63	72	81	90	99	108
	GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC GTG CGG GGC TGC GTG ACC CAG					
	---	---	---	---	---	---
	Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln					
	117	126	135	144	153	162
	AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG ACC TTC TGC TTG CTG GTG					
	---	---	---	---	---	---
	Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Thr Phe Cys Leu Leu Val					
	171	180	189	198		
	GTG GTC GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'					
	---	---	---	---	---	---
	Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr					

FIG. 2

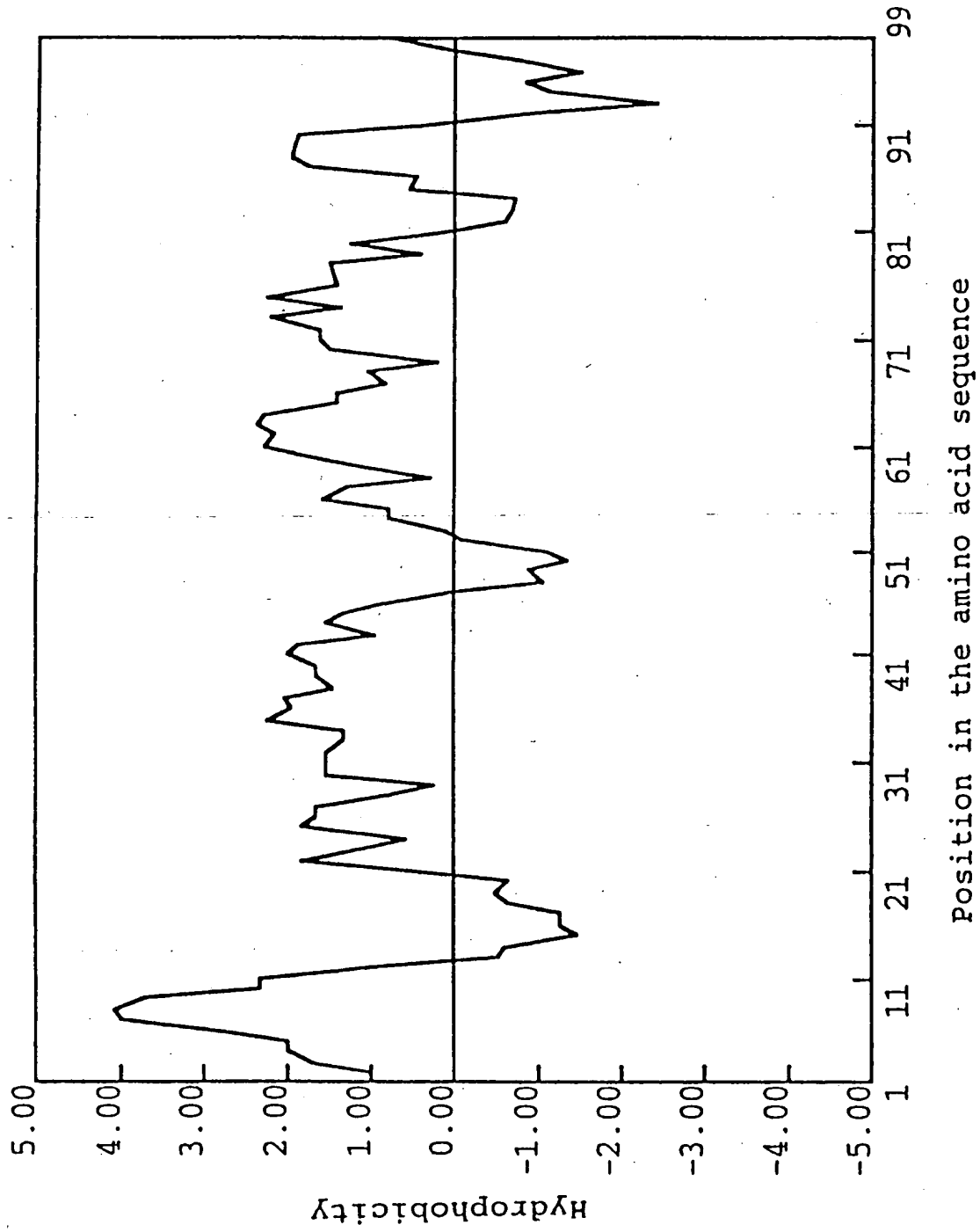


FIG. 3

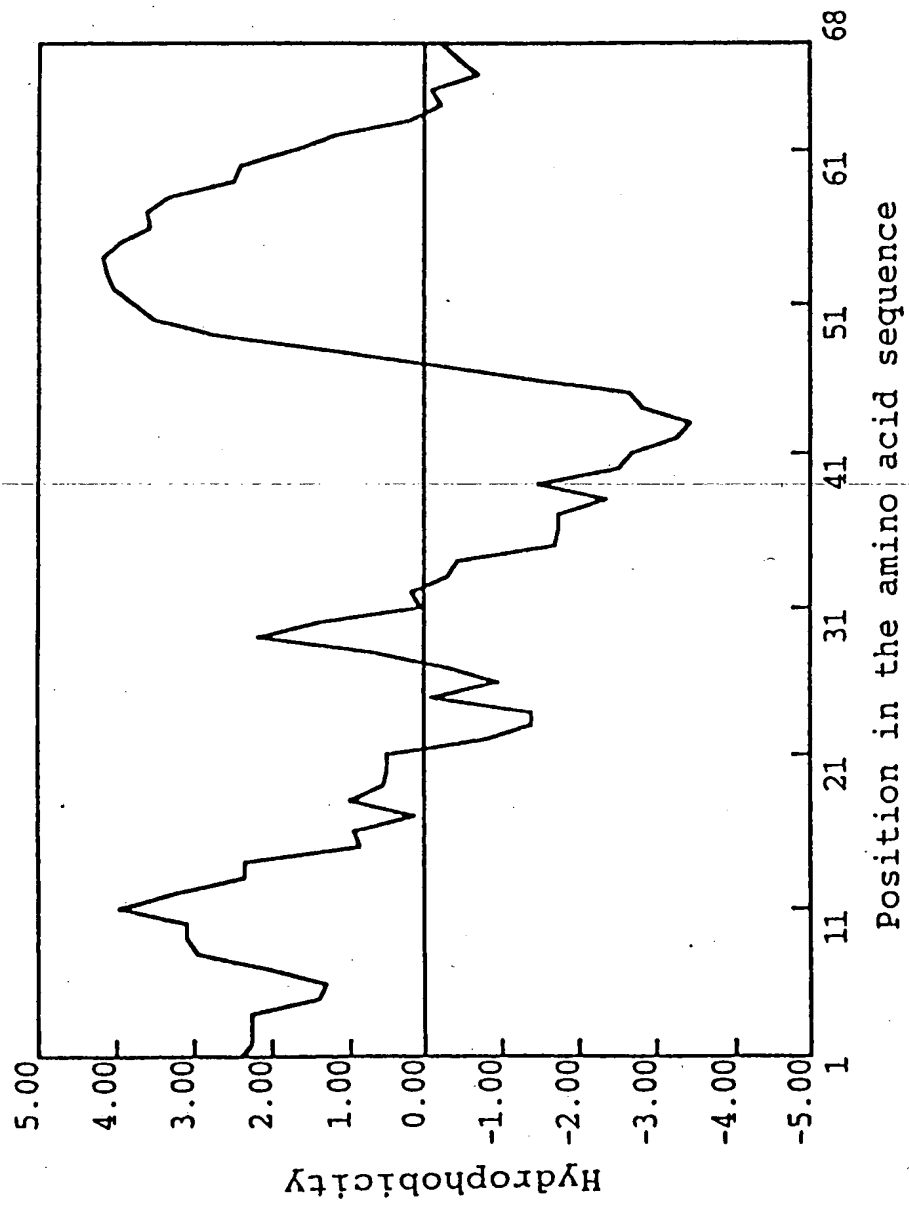


FIG. 4

p19P2	1	VGMVGNVL	LV	LV	IARVRR	LH	NVTN	FLIGNL	ALSD	VL	MCTA	CVPL	TL	AYAF	50			
S12863	1	LGVSGNLA	LI	II	ILKQ	KEMR	NVTN	LIVNL	SFSD	L	VAVM	CLPF	TF	VYTL	50			
p19P2	51	EPRG	WVFG	GG	LCH	LVF	FLQP	VIVY	VS	FTL	TTIA	VD	RYV	LVH	PLRR	RI-	100	
S12863	51	MDH	WV	FGET	MCK	LNP	FVQC	VSIT	VS	IESL	VLIA	VER	HQL	IIN	PRG	WR	REN	100
p19P2	101																	150
S12863	101	NRHAYIGITV	IWV	LAVASSL	PFVI	YQ	ILTD	EPFQ	NV	SLAA	FKDK	YV	CFDK					150
p19P2	151																	200
S12863	151	FPSDSHR	LSY	TYLL	PL	LVIL	LS	VRVS	VK	LRNR	VVPG	CV	TQ	SQ				200
p19P2	201	ADWDRARR	RR	TFC	LL	VVVV	VFAI	CW	LP	YY								250
S12863	201	KYRSSE	TKRI	NVM	LL	SI	VVA	-FAV	CW	LP	LT							250

FIG. 5

171	180	189	198	207	216
TGG GTG TTC GGC GGC CTG TGC CAC CTG GTC TTC CTG CAG GCG GTC ACC					
---	---	---	---	---	---
Trp Val Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr					
225	234	243	252	261	270
GTC TAT GTG TCG GTG TGC ACC CTC ACC ATC GCA GTG GAC CCG TAC GTC GTG					
---	---	---	---	---	---
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr					
279	288	297	306	315	324
CTG GTG CAC CCG CTG AGG CCG CCG ATC TCG CTG CCG CTC AGC GCG TAC GCT GTG					
---	---	---	---	---	---
Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val					
333	342	351	360	369	378
CTG GCC ATC TCG GTG CTG TCC GCG GTG CTG GCG CTG CCC GCG GCG GTC CAC ACC					
---	---	---	---	---	---
Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr					
387	396	405	414	423	432
TAT CAC GTG GAG CTC AAG CCG CAC GAC GTC GCG CTC TCC GAG GAG TTC TGG GCG					
---	---	---	---	---	---
Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Phe Trp Gly					

FIG. 6B

441	450	459	468	477	486
TCC CAG GAG CGC CAG CGC CAG CTC TAC GCC TGG GGG CTG CTG CTG GTC ACC TAC					
---	---	---	---	---	---
Ser Gln Glu Arg Gln Arg Gln Leu Tyr Ala Trp Gly Leu Leu Val Thr Tyr					
495	504	513	522	531	540
CTG CTC CCT CTG CTG ATC CTC CTG TCT TAC GCC CGG GTG TCA GTG AAG CTC					
---	---	---	---	---	---
Leu Leu Pro Leu Leu Val Ile Leu Ser Tyr Ala Arg Val Ser Val Lys Leu					
549	558	567	576	585	594
CGC AAC CGC GTG GTG CCG GGC CGC CTC ACC CAG AGC CAG GCC GAC TGG GAC CGC					
---	---	---	---	---	---
Arg Asn Arg Val Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg					
603	612	621	630	639	648
GCT CGG CGC CGC ACC TTC TTC TGC CTG CTG GTG GTG CTC GTG GTG TTC ACC					
---	---	---	---	---	---
Ala Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Phe Thr					
657	666				
CTC TGC TGC CTG CCC TTC TTC 3'					
---	---	---	---	---	---
Leu Cys Trp Leu Pro Phe Phe					

FIG. 6C

	10	20	30	40	50		
p19P2	1	VGMVGNVLLV	LVIAVRRLH	NVTNFIIGNL	ALSDVLMCTA	CVPLTLAYAF	50
pg3-2/pg1-10	1	VGMVGNILLV	LVIAVRRLY	NVTNFIIGNL	ALSDVLMCTA	CVPLTLAYAF	50
p19P2	51	EPRGMVFGGG	LCHLVFFLQP	VTVVVSVFLL	TTIAVDTRYVV	LVHPLRRRI-	100
pg3-2/pg1-10	51	EPRGMVFGGG	LCHLVFFLQA	VTVVVSVFLL	TTIAVDTRYVV	LVHPLRRRIS	100
p19P2	101	-----	-----	-----	-----	-----	150
pg3-2/pg1-10	101	LRLSAYAVLA	IWLSAVLAL	PAAVHTYHVE	LKPHDVRICE	EFWGSQERQR	150
p19P2	151	-----GLLLV	TYLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSQADWDRAR	200
pg3-2/pg1-10	151	QLYAWGLLV	TYLLPLLVIL	LSYVRVSVKL	RNRVVPGRVT	QSQADWDRAR	200
p19P2	201	RRRTFCLLV	VVVVFALCWL	PXY.....	250
pg3-2/pg1-10	201	RRRTFCLLV	VVVVFILCWL	PFF.....	250

FIG. 7

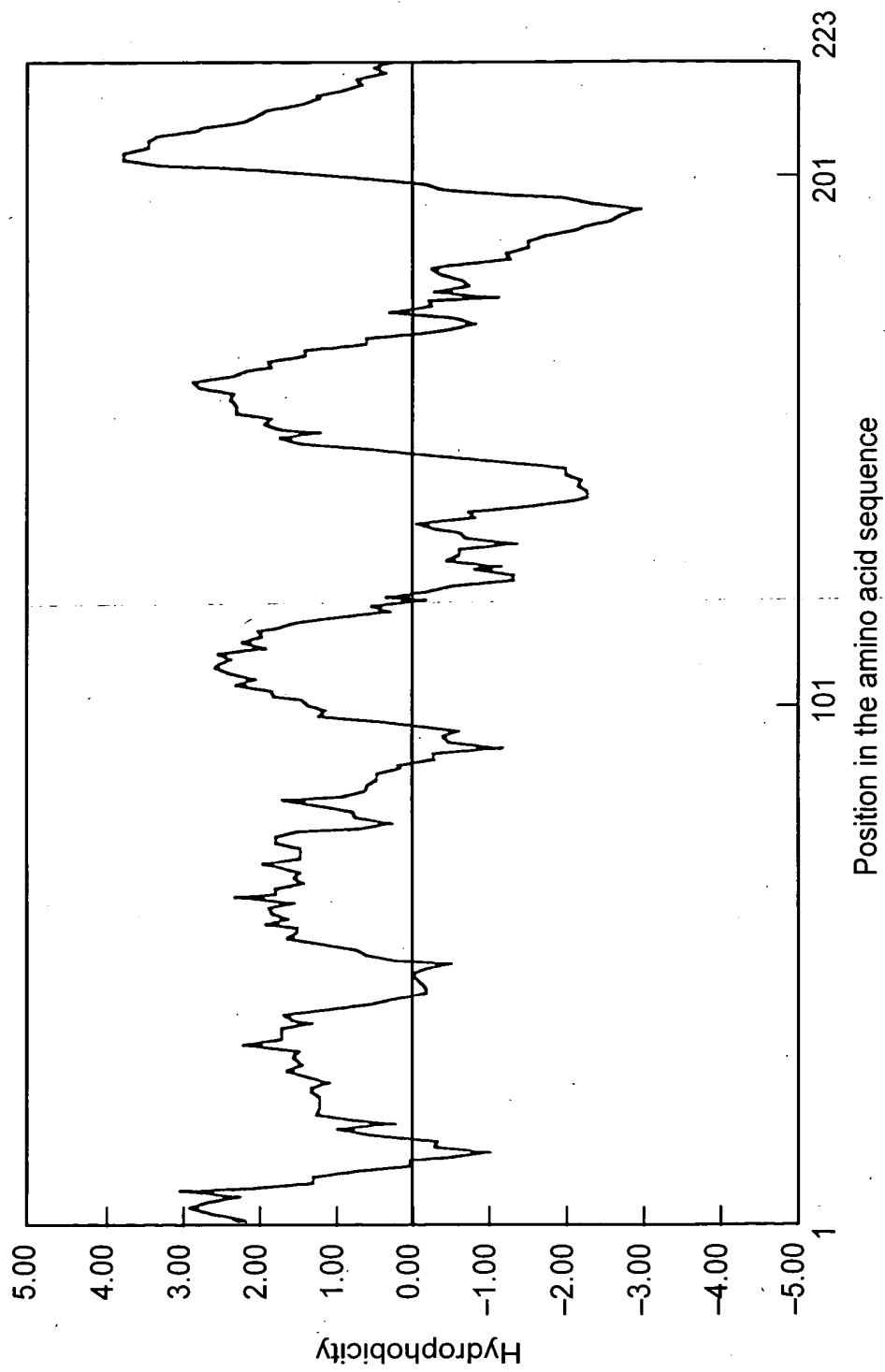


FIG. 8

FIG. 9A
FIG. 9B
FIG. 9C

FIG. 9

1 CATCGTCAAGCAGATGAAGATCATCCACGAGATGGCTACTCCGAGGCCAGCAGAAATT 60
 1
 61 CTGCCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAACCCCACTCCAGGTGGCCATG 120
 1 Met
 121 GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGTGCCCGCGCG 180
 1 AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla 21
 181 GTCACAACTCCGCCCAACGAGCGCAGAGGCCTCGCGCGCAACGGGTCTGGTGGTGGC 240
 21 ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly 41
 241 GCGGACGCTCCAGCCGTACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGG 300
 41 AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly 61

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FIG. 9A

301	CTGATCGTGTGCTCTACAGCGTGTGTTGGTGGCTGGTGGCACTGCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTGATCGCGGGTGGCGCTGCACACGTGACGAACCTTCTCATCGGCAAC	420
81	ValLeuValIleAlaArgValArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTGTCCGACGTGCTCATGTGCACCGCTGCGTCCGCTCACGCTGCGCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTCGAGCCACGGCGTGGTGTTCGGCGCGCGCTGTGCCACCTGGTCTTCTTCCTGCAG	540
121	PheGluProArgGlyTyrValPheGlyGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGGTCACCGTCTATGTGTGGTGTTCACGCTCACCAACCATCGCAGTGGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGACCCGCTGAGCGCGCATCTCGCTCGCCCTACGCCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGCGCTGTCCGGGTGCTGGCGTCCCGCCGCTGCACACCTATCAGCTG	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTCGGAGGAGTCTGGGCTCCAGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCTGGGGCTGTGTGTGTGTCACCTACCTGCTCCCTCTGCTGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241

FIG. 9B

841	CTCCTGTCTTACGTCCGGGTGTCAGTAAAGTCCGCAACCGGTGGTGGCCGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGCCGACTGGGACCGCGCTCGCGCCGCGCACCTTCTGCTTGTGCTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCGTGCTGTTCCCGCTCTGCTGGCTGCCGTGCACGTCTTCAACCTGCTGCGG	1020
281	ValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCAAGCCATCGACCCCTTACGCCCTTTGGGCTGGTGCAGCTGCTCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTCGGCCTGCTACAACCCCTTCACTACGCTGGCTGCACGACAGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCGGCGAGAGCTGGCAACTGTTGGTGGCTTGGCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAATATGACCGTCAGCGTGTCTATCTGATGCCACTTAGCCAGGCCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGCGCACCACCTCGAGGTCAATCTGTGCTTATTCTCAGCA	1320
371		371
1321	CCAGAGCTAGC	1331
371		371

FIG. 9C

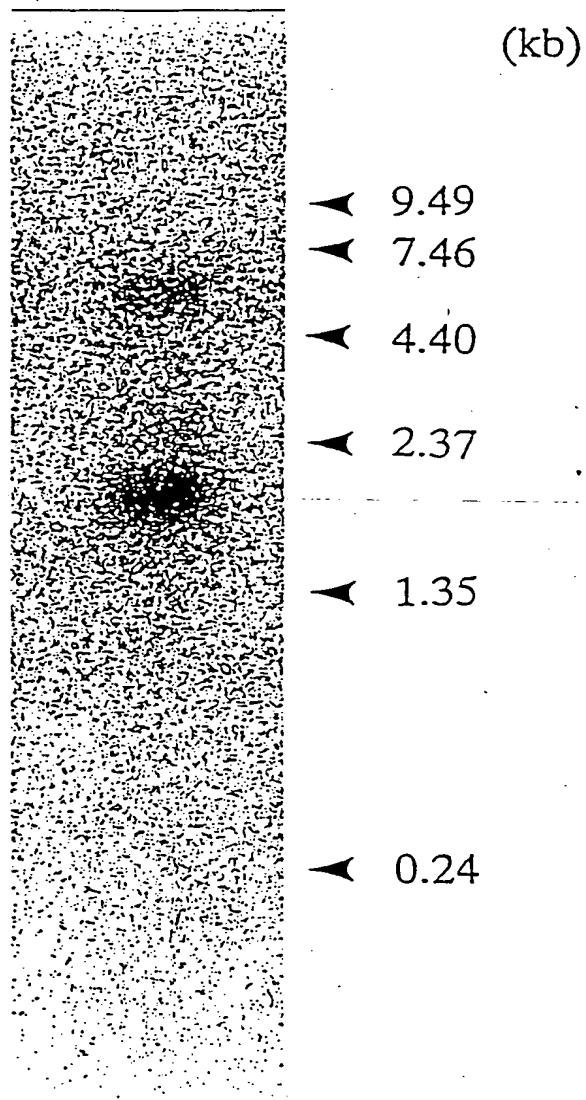


FIG. 10

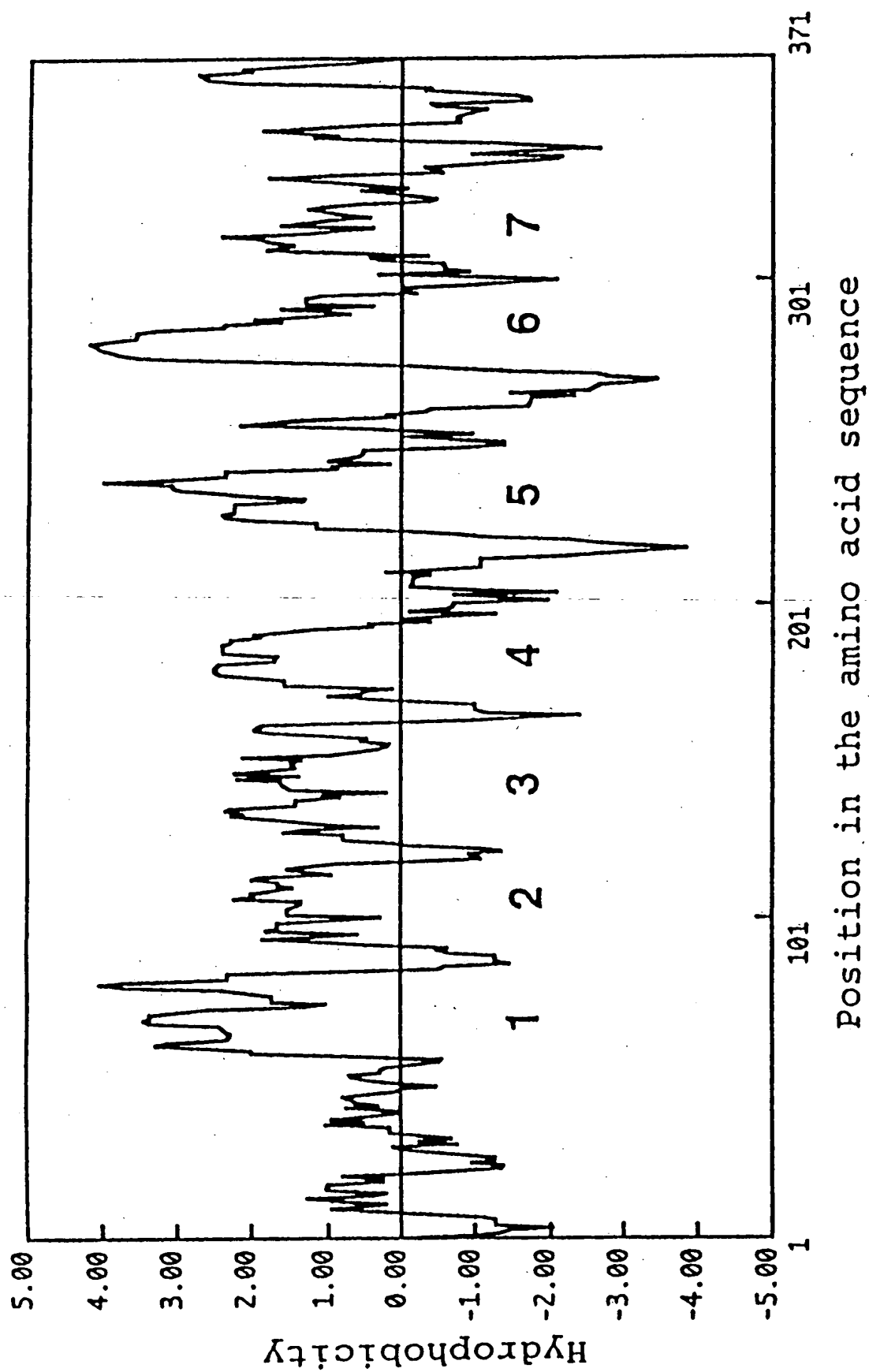


FIG. 11

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		9		18		27		36		45		54						
5'	CTG	TGT	GTC	ATC	CCG	GTG	GAT	AGG	TAC	GTG	GTT	CTG	GTG	CAC	CCG	CTA	CGT	CCG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Cys	Val	Ile	Ala	Val	Asp	Arg	Tyr	Val	Val	Leu	Val	His	Pro	Leu	Arg	Arg
			63		72		81		90		99		108					
	CGC	ATT	TCA	CTG	AGG	CTC	AGC	GCC	TAC	GCG	GTG	CTG	GGC	ATC	TGG	GCT	CTA	TCT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Ile	Ser	Leu	Arg	Leu	Ser	Ala	Tyr	Ala	Val	Leu	Gly	Ile	Trp	Ala	Leu	Ser
			117		126		135		144		153		162					
	GCA	GTG	CTG	GCG	CTG	CCG	GCC	GCG	GTG	CAC	ACC	TAC	CAT	GTG	GAG	CTC	AAG	CCC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ala	Val	Leu	Ala	Leu	Pro	Ala	Ala	Val	His	Thr	Tyr	His	Val	Glu	Leu	Lys	Pro
			171		180		189		198		207		216					
	CAC	GAC	GTG	AGC	CTC	TGC	GAG	GAG	TTC	TGG	GCG	TCG	CAG	GAG	CGC	CAA	CGC	CAG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	His	Asp	Val	Ser	Leu	Cys	Glu	Glu	Phe	Trp	Gly	Ser	Gln	Glu	Arg	Gln	Arg	Gln
			225		234		243		252		261		270					
	ATC	TAC	GCC	TGG	GGG	CTG	CTT	CTG	GCG	ACC	TAT	TTG	CTC	CCC	CTG	CTG	GCC	ATC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ile	Tyr	Ala	Trp	Gly	Leu	Leu	Leu	Gly	Thr	Tyr	Leu	Leu	Pro	Leu	Leu	Ala	Ile
			279		288		297		306		315		324					
	CTC	CTG	TCT	TAC	GTA	CGG	GTG	TCA	GTG	AAG	CTG	AGG	AAC	CGC	GTG	GTG	CCT	GGC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Leu	Ser	Tyr	Val	Arg	Val	Ser	Val	Lys	Leu	Arg	Asn	Arg	Val	Val	Pro	Gly
			333		342		351		360		369		378					
	AGC	GTG	ACC	CAG	AGT	CAA	GCT	GAC	TGG	GAC	CGA	GCG	CGT	CGC	CGC	CGC	ACT	TTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Ser	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Asp	Arg	Ala	Arg	Arg	Arg	Arg	Thr	Phe
			387		396		405		414		423		432					
	TGT	CTG	CTG	GTG	GTG	GTG	GTA	GTG	TTC	ACG	CTC	TGC	TGG	CTG	CCC	TTC	TAC	
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Cys	Leu	Leu	Val	Val	Val	Val	Val	Phe	Thr	Leu	Cys	Trp	Leu	Pro	Phe	Tyr	

CT 3'

--
—

FIG. 12

p19P2	1	VGMVGNVLLV	10	LVIAVRRLH	20	NVTNFLIGNL	30	ALSDVLMCTA	40	CVPLTLAYAF	50	
pG3-2/pG1-10	1	VGMVGNVLLV		LVIAVRRLY		NVTNFLIGNL		ALSDVLMCTA		CVPLTLAYAF		50
p5S38	-79		-30
p19P2	51	EPRGMVFGGG	60	LCHLVFFLQP	70	VTYVVSFVTL	80	TTIAVDRIYV	90	LVHPLRRRI	100	
pG3-2/pG1-10	51	EPRGMVFGGG		LCHLVFFLQA		VTYVVSFVTL		TTIAVDRIYV		LVHPLRRRI		100
p5S38	-29		CVIAVDRIYV		LVHPLRRRI		21
p19P2	101	-----	110	120		130		140		150		
pG3-2/pG1-10	101	LRLSAYAVLA		IMVLSAVLAL		PAAVHTYHVE		LKPHDVRICE		EFWGSQERQR		150
p5S38	22	LRLSAYAVLG		IMVLSAVLAL		PAAVHTYHVE		LKPHDVSLCE		EFWGSQERQR		71
p19P2	151	-----GLLLV	160	170		180		190		200		
pG3-2/pG1-10	151	QLYANGLLLV		TYLLPLLVIL		LSYVRVSVKL		RNRVVFQCVT		QSQADWDRAR		200
p5S38	72	QIYANGLLLG		TYLLPLLAII		LSYVRVSVKL		RNRVVFQSVT		QSQADWDRAR		121
p19P2	201	RRRTFCLLLV	210	220		230		240		250		
pG3-2/pG1-10	201	RRRTFCLLLV		VVVFALCWL		PVY.....			250
p5S38	122	RRRTFCLLLV		VVVFALCWL		PVY.....			171

FIG. 13

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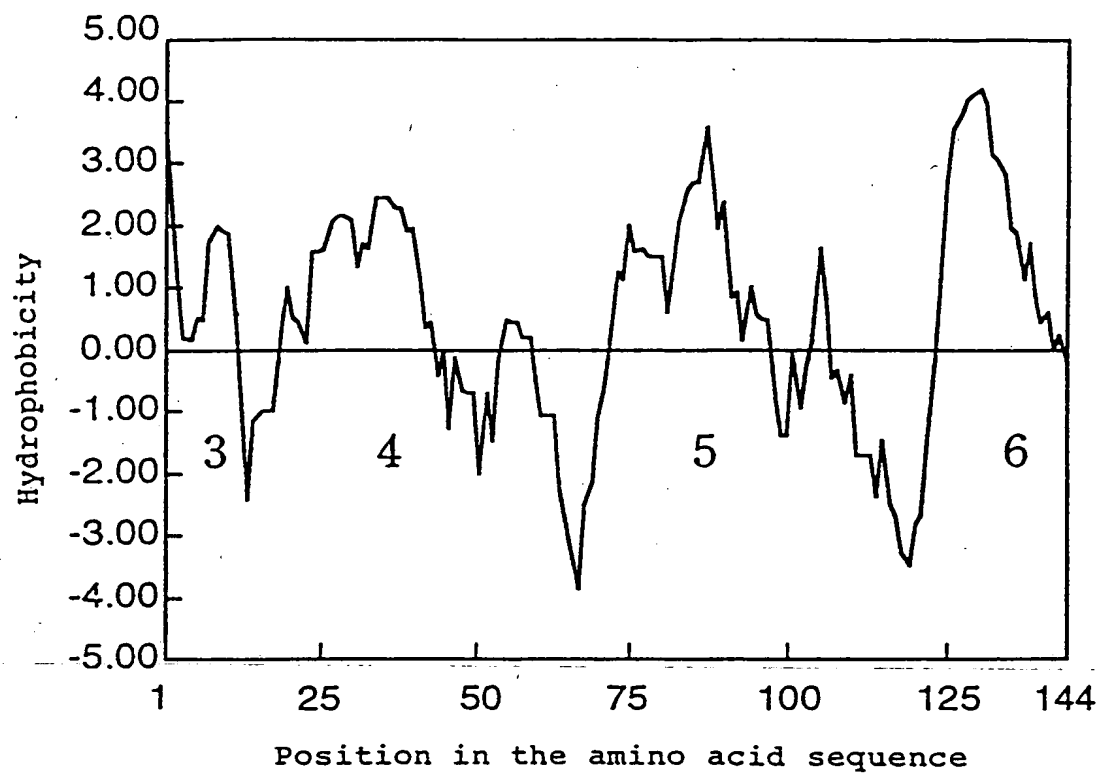


FIG. 14

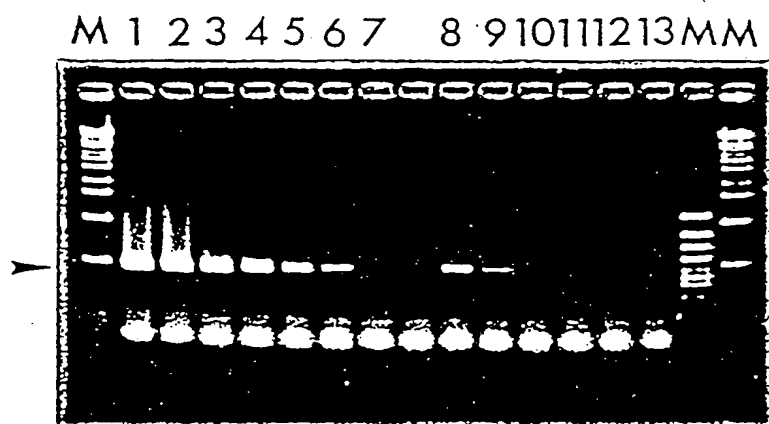


FIG. 15

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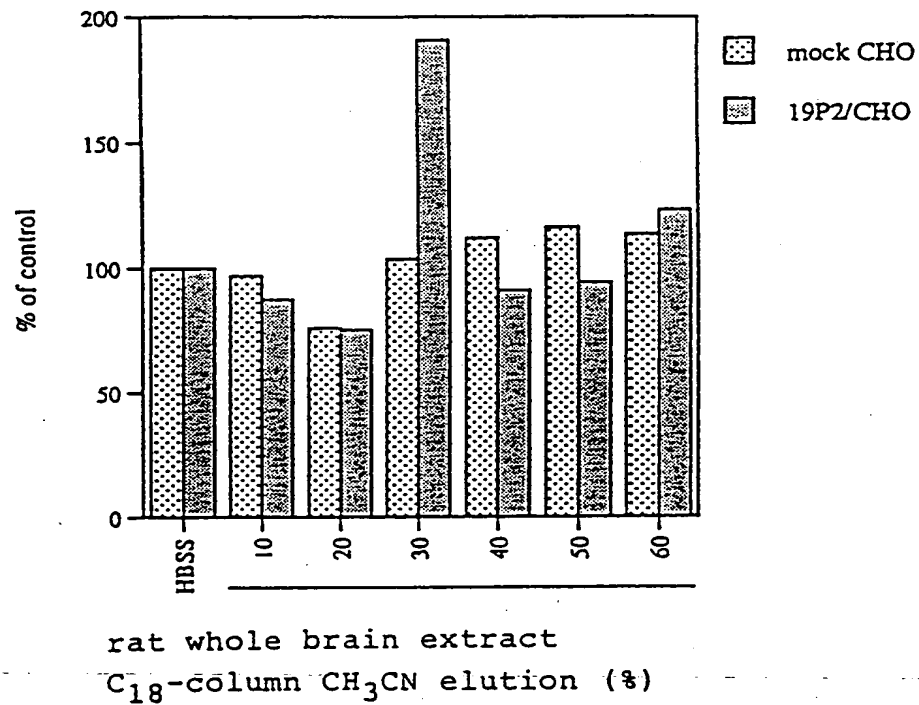


FIG. 16

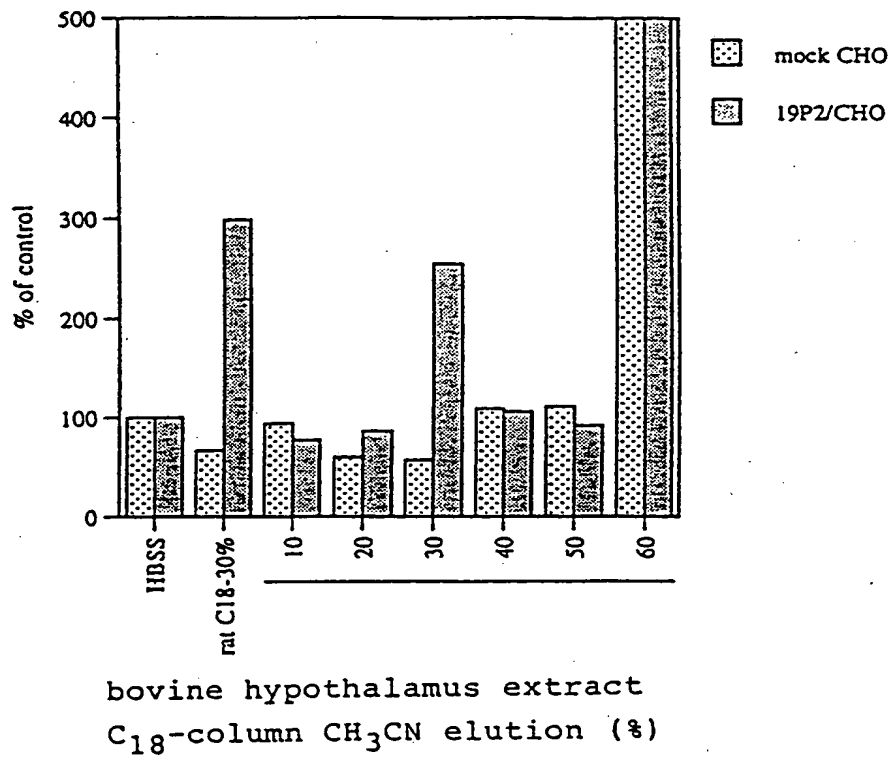


FIG. 17

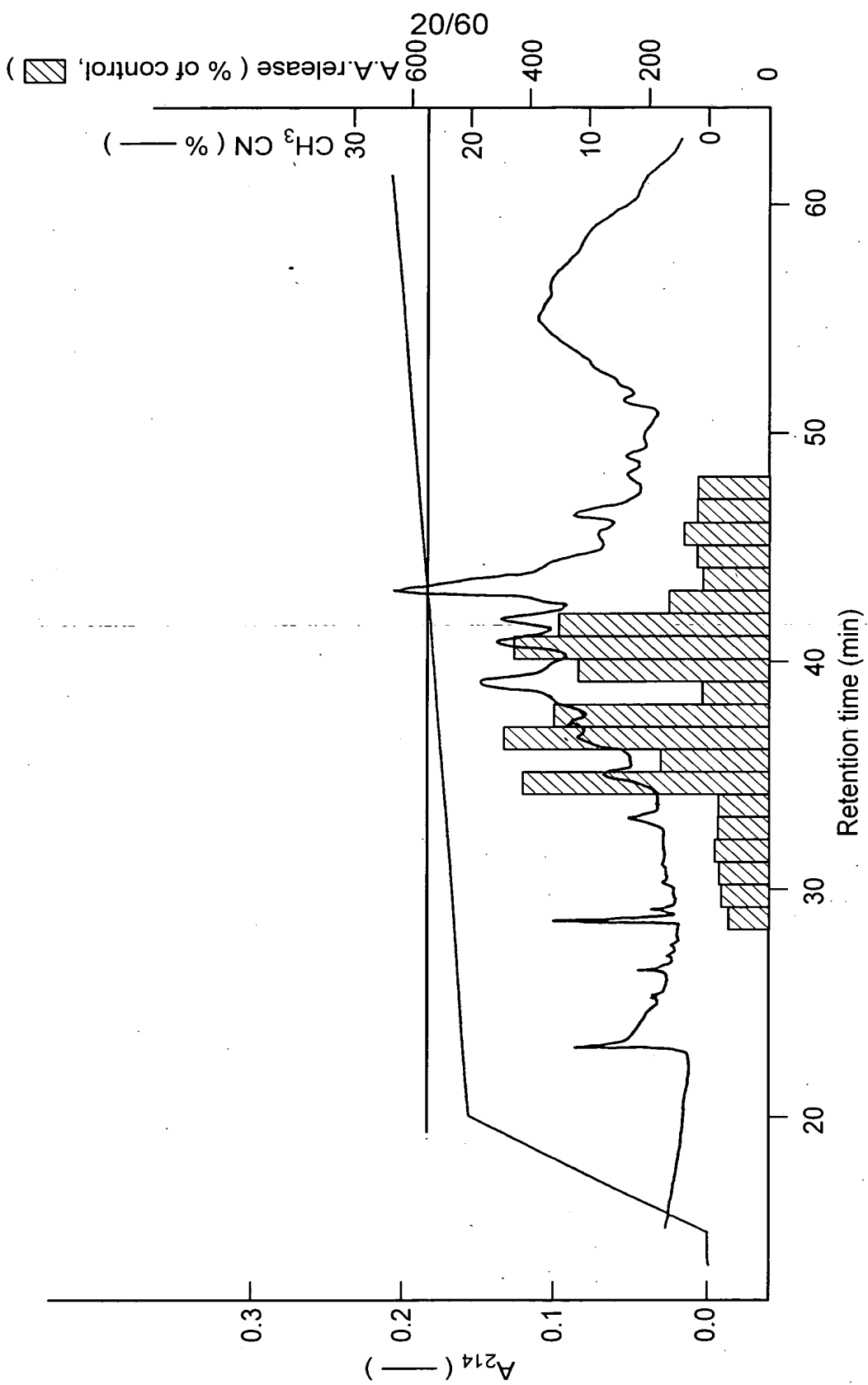
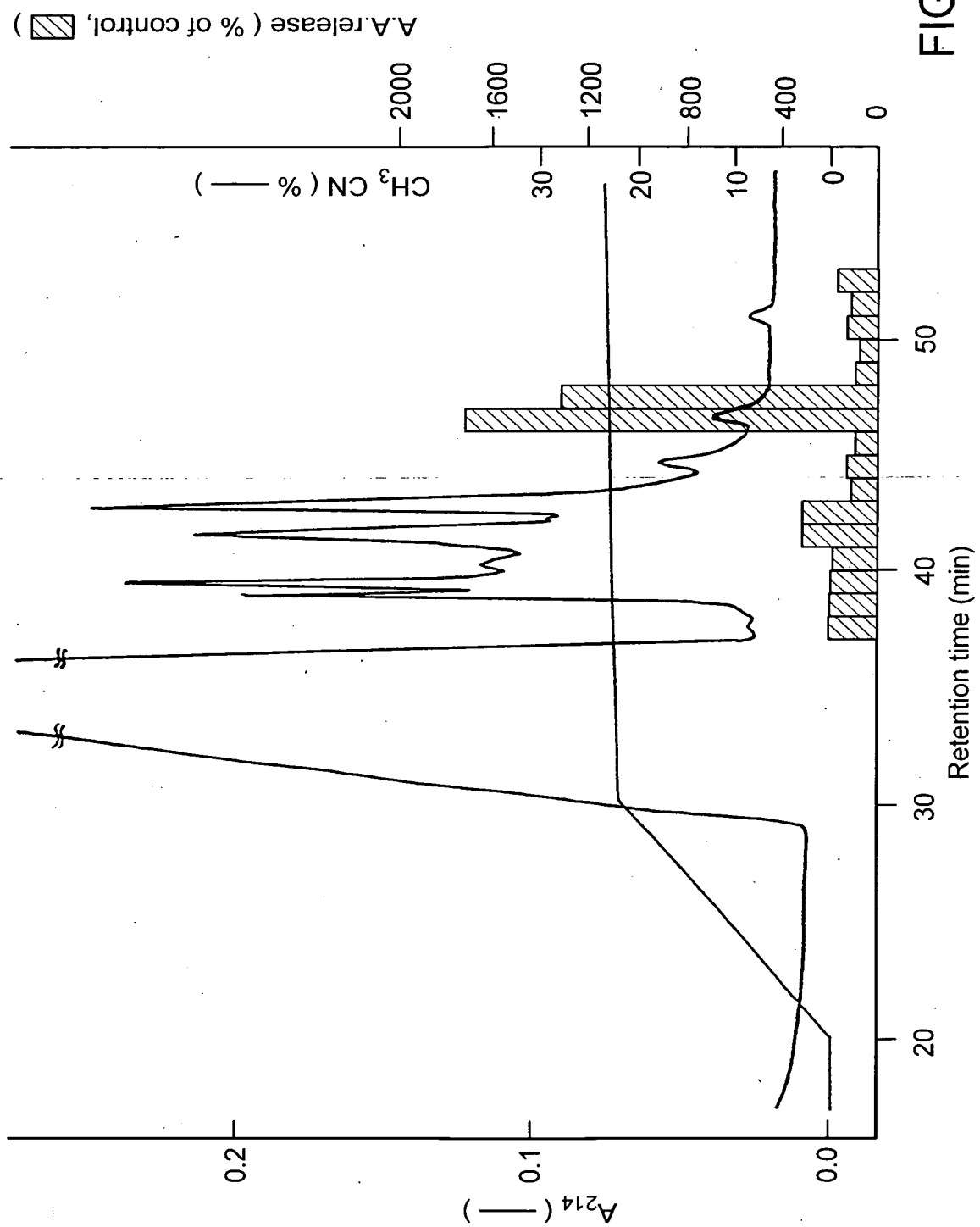


FIG. 18



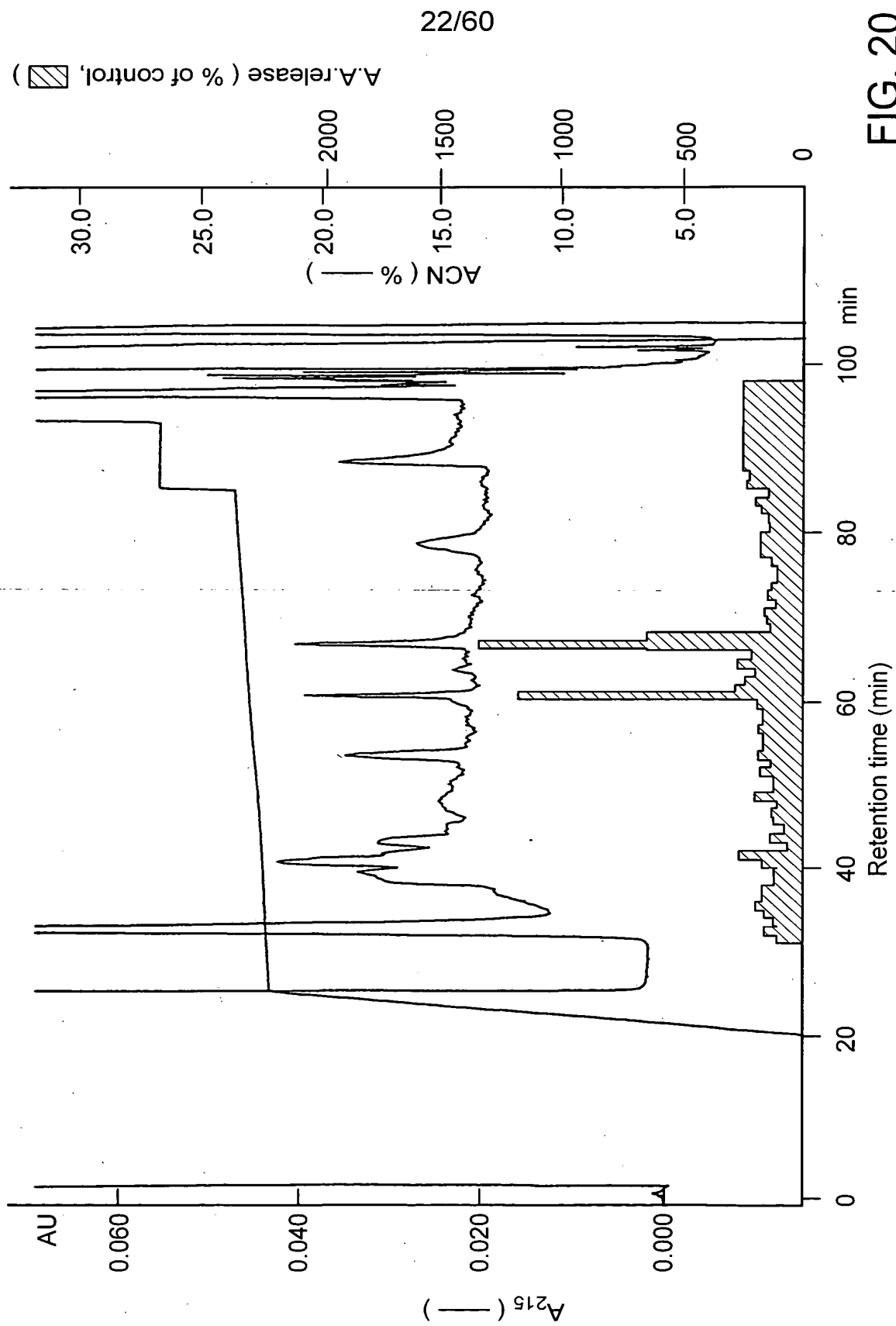


FIG. 20

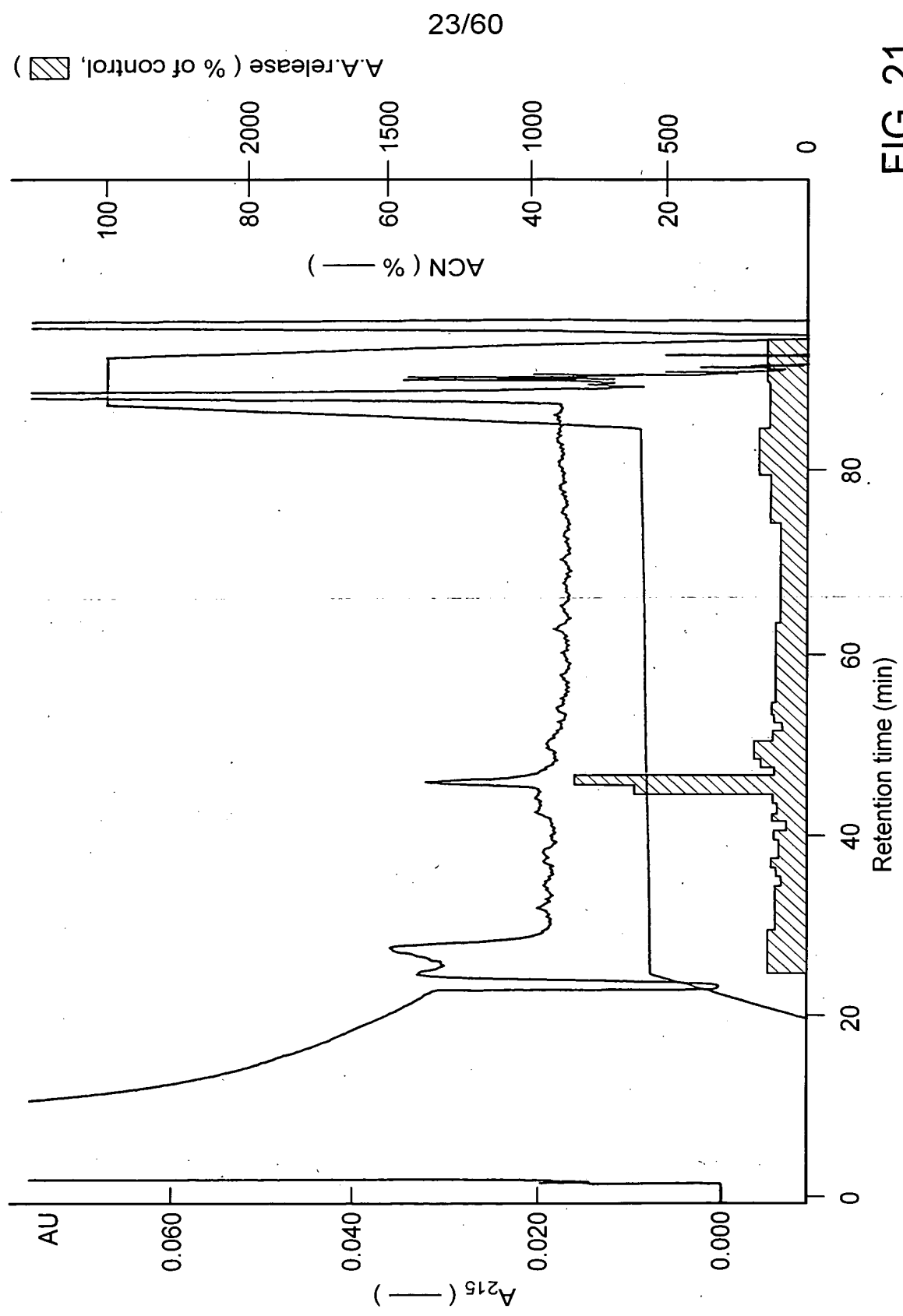


FIG. 21

P5-1

	9	18	27	36	45	54
5'	GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC ATC AAC CCT GCC TGG TAC					
	---	---	---	---	---	---
	Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr					↓

63 72

GCG GGC CGT GGG ATC CGG CCC G 3'

Ala Gly Arg Gly Ile Arg Pro

P3-2

FIG. 22

1	GTGGAATGAAGCGGTGGGGCTGGCTCCTCTGCTGCTGCTGGCCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGGCTGCCAGAGAGCCACAGCACTCCATGGAGATCCGCACCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
	↓	
	PDN	
120	CCTGCCT	126
39	ProAla	40

FIG. 23

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1	GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCCTGCTGCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGCTGCCAGCAGAGCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGCCGCTTCGGCCGGCAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla	58
180	GCCCCGGGACGACCCAGGCCTGGCCCCCGCGTGTGCCGGCCTGCTTCCGCCCTGGAA	239
59	AlaProGlyAspGlyProArgProGlyProArgValProAlaCysPheArgLeuGlu	78
240	GGCGYGCTGAGCCCTCCCGAGCCCTCCCGGGCGGCTGACGGCCAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAACAGCGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT	359
		98
360	AATAAAAGCAGCTGGCTTGTT	380
		98

FIG. 24A

1 GTGGAATGAAGCGGTGGGGCCTGGCTCCTCTGCTGCTGCTGCTGGCCTGGCCCTG 59
 1 MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu 18
 60 CAGGGGGCTGCCAGCAGAGCCCCACCAGCACTCCATGGAGATCCGCCACCCCCGACATCAAC 119
 19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn 38
 120 CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCGTGGCCCGCTTCGGCCGCGAAGAGCT 179
 39 ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla 58
 180 GCCCTGGGGACGACCCAGGCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCCTGGAA 239
 59 AlaLeuGlyAspGlyProArgProGlyProArgValProAlaCysPheArgLeuGlu 78
 240 GGCGGYGCTGAGCCCTCCCGAGCCCTCCGGGGGGCTGACGGCCAGCTGGTCCAGGAA 299
 79 GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu 98
 300 TAACAGCGGAGCCTGCCCCCCCCACCCCTCCTCCACCAGCCACCTTCCCTCCAGTCCT 359
 98
 360 AATAAAGCAGCTGGCTTGTT 380
 98

FIG. 24B

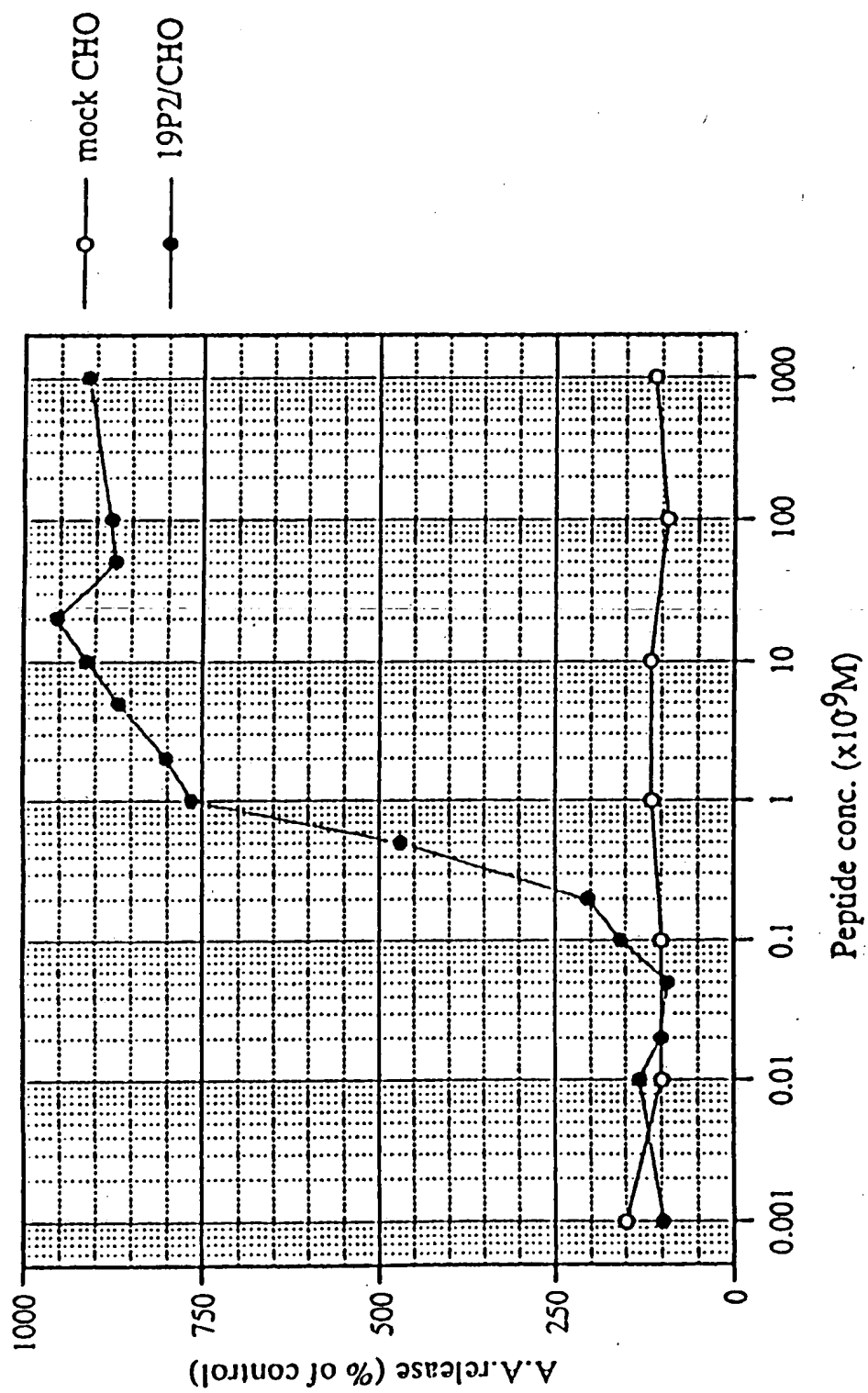


FIG. 25

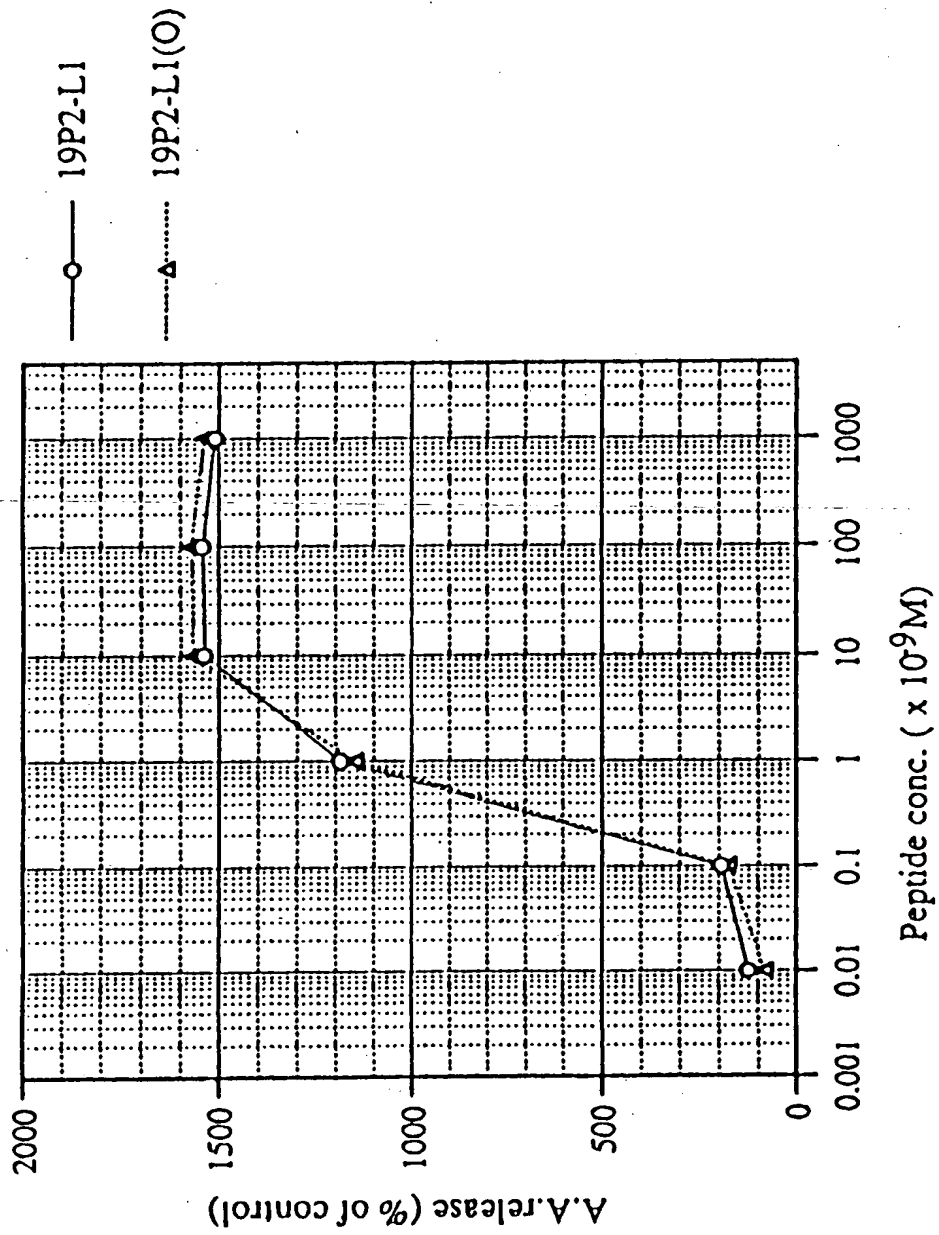


FIG. 26

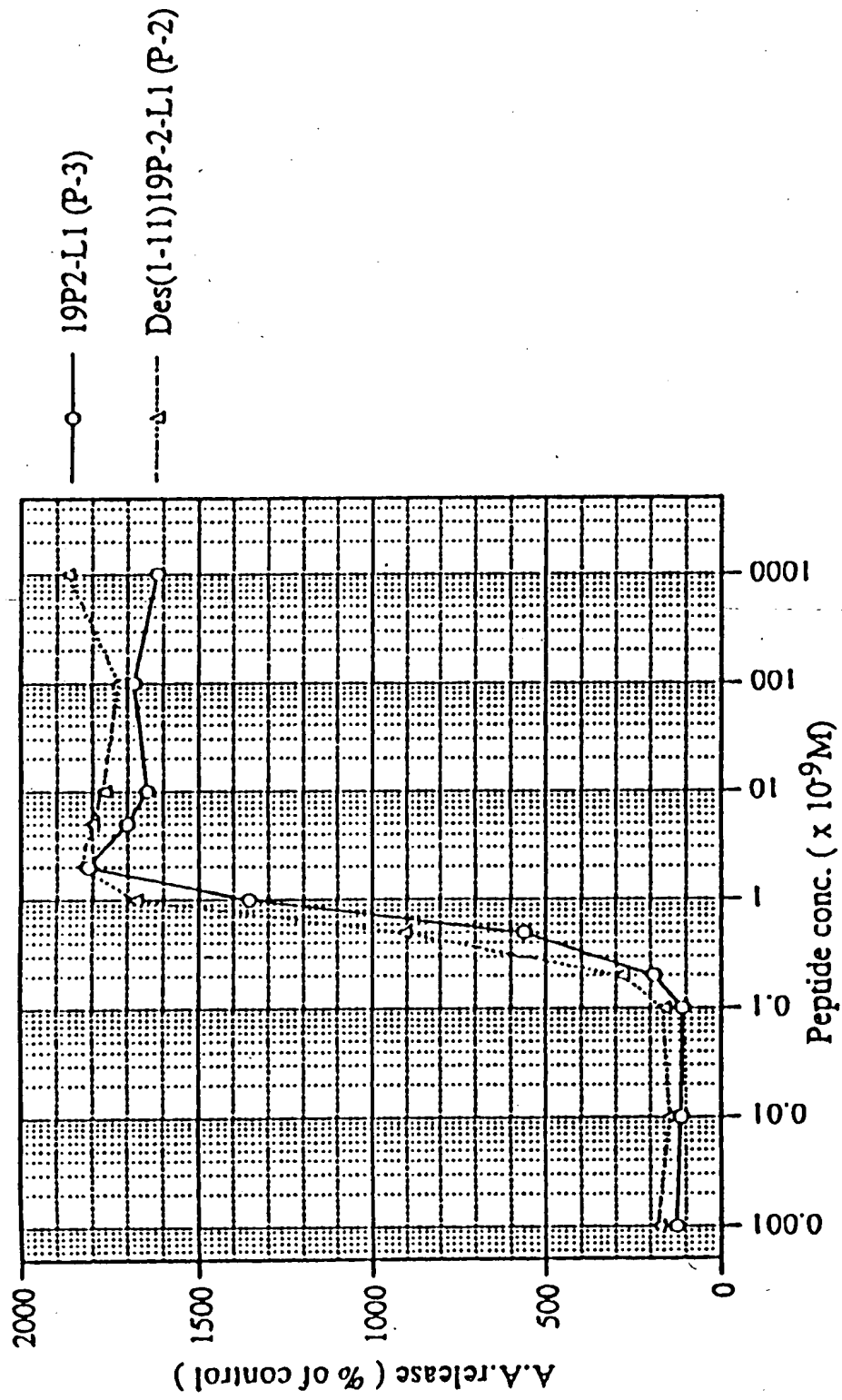


FIG. 27

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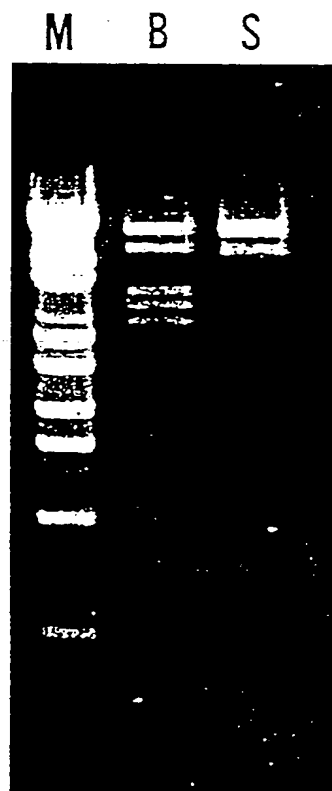


FIG. 28

10	20	30	40	50	60
ATGAAGGCGG	TGGGGGCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTGGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTCCCCCAG	GTGGCCCCGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.

FIG. 29

FIG. 30A
FIG. 30B
FIG. 30C

FIG. 30

genome cDNA	1	ATGAAGCGG	TGGGGGCTG	GCTCCTCTG	CTGCTGCTG	TGGGCTGGC	50
	1	ATGAAGCGG	TGGGGGCTG	GCTCCTCTG	CTGCTGCTG	TGGGCTGGC	50
genome cDNA	51	CCTGCAGGG	GCTGCCAGCA	GAGCCACCA	GCACTCCATG	GAGATCCGCA	100
	51	CCTGCAGGG	GCTGCCAGCA	GAGCCACCA	GCACTCCATG	GAGATCCGCA	100
genome cDNA	101	GTGAGTGTCT	AGCCCCGCCC	CTGCCCCCAG	GGTTCACAGG	GGGGCCTGG	150
	101	-----	-----	-----	-----	-----	150
genome cDNA	151	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA	GCATCCTGGG	GTGGGGTTT	200
	151	-----	-----	-----	-----	-----	200

FIG. 30A

genome	201	210	220	230	240	250
		GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA	CAGGTGCTCC
cDNA	201	-----	-----	-----	-----	-----
genome	251	260	270	280	290	300
		CAAGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCCTC	ACCACACGGG
cDNA	251	-----	-----	-----	-----	-----
genome	301	310	320	330	340	350
		TGGCCTGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA
cDNA	301	-----	-----	-----	-----	-----
genome	351	360	370	380	390	400
		GGAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCIGAATC	CTACTTCCCA
cDNA	351	-----	-----	-----	-----	-----
genome	401	410	420	430	440	450
		AAGCCACCC	AGCACCAGAA	ATGGGGCTC	CGGTGAACC	TCCTGTGCGG
cDNA	401	-----	-----	-----	-----	-----
genome	451	460	470	480	490	500
		GTGGGTGGTC	CTGGCATEGC	CTGGGGGACA	GGCAGCCATG	AGCTGAGCAC
cDNA	451	-----	-----	-----	-----	-----

FIG. 30B

genome cDNA	510	520	530	540	550
	501 ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT
genome cDNA	560	570	580	590	600
	551 GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
genome cDNA	610	620	630	640	650
	601 AGGCCGTGGG	ATCCGGCCCG	TGGCCCGCTT	CGGCCGGCGA	AGAGCTGCCC
genome cDNA	660	670	680	690	700
	651 TGGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC
genome cDNA	710	720	730	740	750
	701 CTGGAAGGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC
genome cDNA	760	770	780	790	800
	751 CCAGCTGGTC	CAGGAATAA.
genome cDNA	760	770	780	790	800
	751 CCAGCTGGTC	CAGGAATAA.

FIG. 30C

FIG. 31

FIG. 31

1 GGCATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG 59
 1 MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu 12
 60 CTAAGCTTGGTCCTCCAGGGGCTTCCAGCCGAGCCCAACAGCACTCCATGGAGACAAGA 119
 13 LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg 32
 120 ACCCCTGATATCAATCCTGCCTGGTACACGGCCGCGGATCAGCCCTGTGGCCCGCTTC 179
 33 ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe 52
 180 GGCAGGAGAAGGGCAACCCGAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCCTCCCA 239
 53 GlyArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro 72
 240 CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCAGCTCGAGAAGACAGTGC 299
 73 LeuAspGlyArgThrLysPheSerGlnArgGly*** 83
 300 TGCTGAGCCCAAGCCCACTCCCTGTCCCTGCAGACCCCTCCTTACCCCTCCCTCTCCT 359
 83 83
 360 CTGCT 364
 83 83

FIG. 32

bovine.aa	P	G	D	G	P	R	P	G	P	R	R	V	P	A	C	F	R	
		210			220			230				240					250	
bovine.seq	183	CCGGGGGACG	GACCCAGGCC	TGGCCCCCGG	CGTGTGCCGG	CCTGCTTCCG											232	
rat.seq	201	CCGAGGGATG	TCACTGGACT	TGGC-----	----CAACTCA	GCTGCCCTCCC											250	
bovine.aa	L	E	G	G	A	E	P	S	R	A	L	P	G	R	L	T	A	
		260			270			280				290					300	
bovine.seq	233	CCTGGAAGGC	GGCGCTGAGC	CCTCCCGAGC	CCTCCCGGGG	CGGCTGACGG											282	
rat.seq	251	ACTGGATGGA	CGCACCAAGT	TCTCTCAGCG	TGGATAACAC	CCCAGCTCGA											300	
bovine.aa	Q	L	V	Q	E	*												
		310			320			330			340						350	
bovine.seq	283	CCCAGCTGGT	CCAGGAATAA	CAGCGGGAGC	CTGCCCCCCA	CCCCCTCCTCC											332	
rat.seq	301	GAAGACAGTG	CTGCTGAGCC	CAAGCCCACA	CTCCCTGTCC	CCTGCAGACC											350	
bovine.aa		360			370			380			390						400	
bovine.seq	333	TCCACCAGCC	ACCTTCCCTC	CAGTCCTAAT	AAAAGCAGCT	GGCTTGTT..											382	
rat.seq	351	CTCCTCTACC	CTCCCTCTCC	TCTGCT....											400	

FIG. 33B

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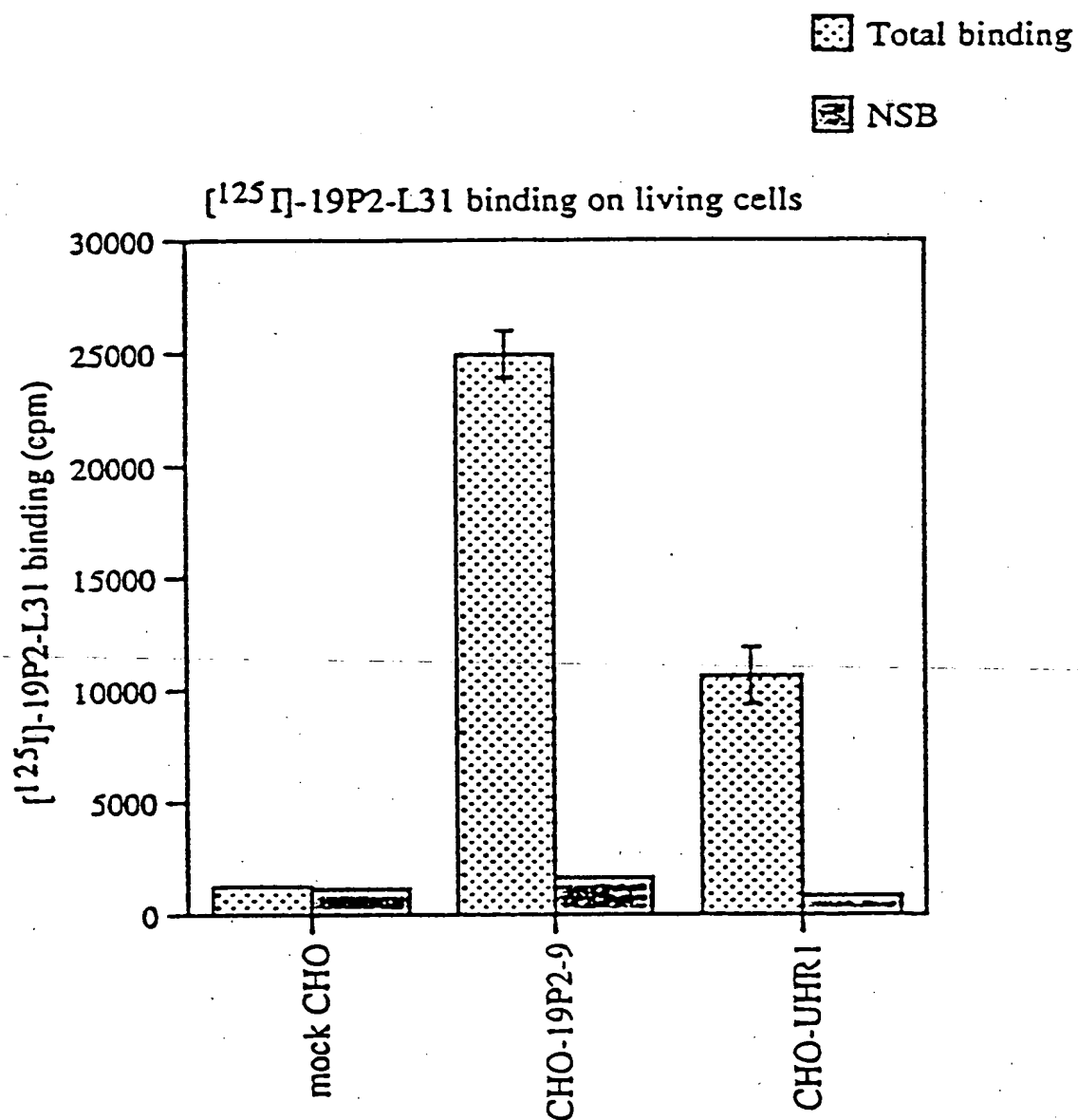
1	GGCCTCCTCGGAGGAGCCAAGGATGAAGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG	59
1	MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu	12
60	ATGCTGGGCCTGGCCCTGCGGGAGCTGCAAGTCGTACCCATCGGCACCTCCATGGAGATC	119
13	MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle	32
120	CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGGATCAGGCCCTGTGGGCCGC	179
33	ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg	52
180	TTCGGTCGGAGGAGGCAACCCCTGGGGACGTCCCCAAGCCTGGCCTGCGACCCCGGCTG	239
53	PheGlyArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu	72
240	ACCTGCTTCCCCCTGGAAGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCTTGT	299
73	ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly***	87
300	CAAGAAACTCACTCTGGAGCCTCCCCCACCACCCCTCTCCTCTCCTTCGGGCTCCTTTC	359
87		87
360	CC	361
87		87

FIG. 34

		10	20	30	40	50	
bovine.aa	1	MKAVGAWLLC	LLLLGLALQG	AASRAHQHSM	EIRTPDINPA	WYAGRGIRPV	50
rat.aa	1	M-ALKTWLLC	LLLLSLVLPG	ASSRAHQHSM	ETRTPDINPA	WYTGRGIRPV	50
human.aa	1	MKVLRAWLLC	LIMLGALRG	AASRTHRHSM	EIRTPDINPA	WYASRGIREV	50
		60	70	80	90	100	
bovine.aa	51	GRFGRRRAAP	GDGERPGPRR	VPACFRLEGG	AEPSRALPGR	LTAQLVQE*	100
rat.aa	51	GRFGRRRATP	RDVTGLG---	QLSCLPLDGR	TKFSQRG*	100
human.aa	51	GRFGRRRATL	GDVFKFGLRP	RLTCFPLEGG	AMSSQDG*	100

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FIG. 35



cells; 0.5×10^7 cells/ml

$[^{125}\text{I}]\text{-19P2-L31}$; 200pM (avg. 63857.3cpm)

NSB; 200nM (x 1,000)

reaction; RT, 2.5hr

in HBSS + 0.05% BSA + 0.05% CHAPS

in 100 μl

FIG. 36

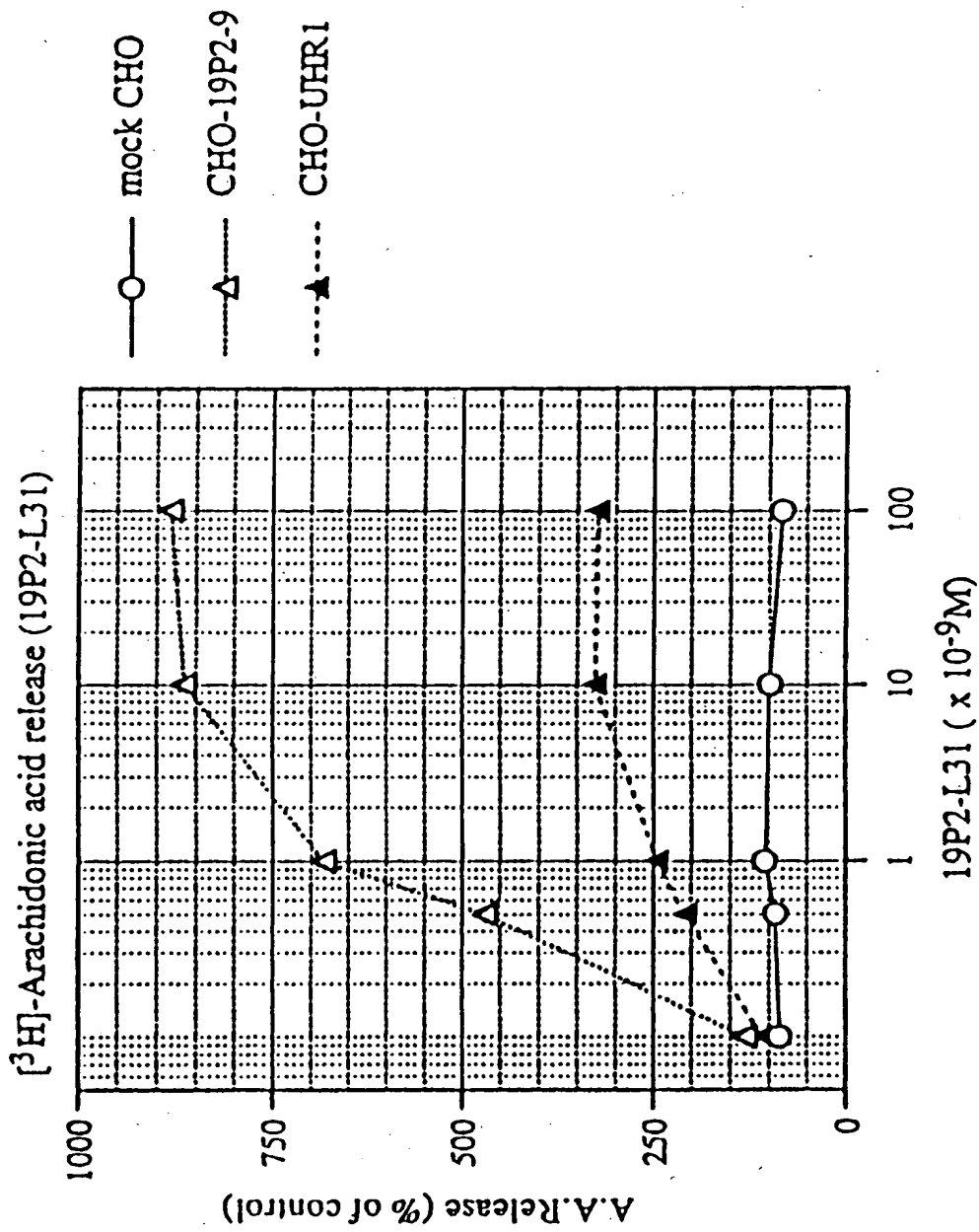


FIG. 37

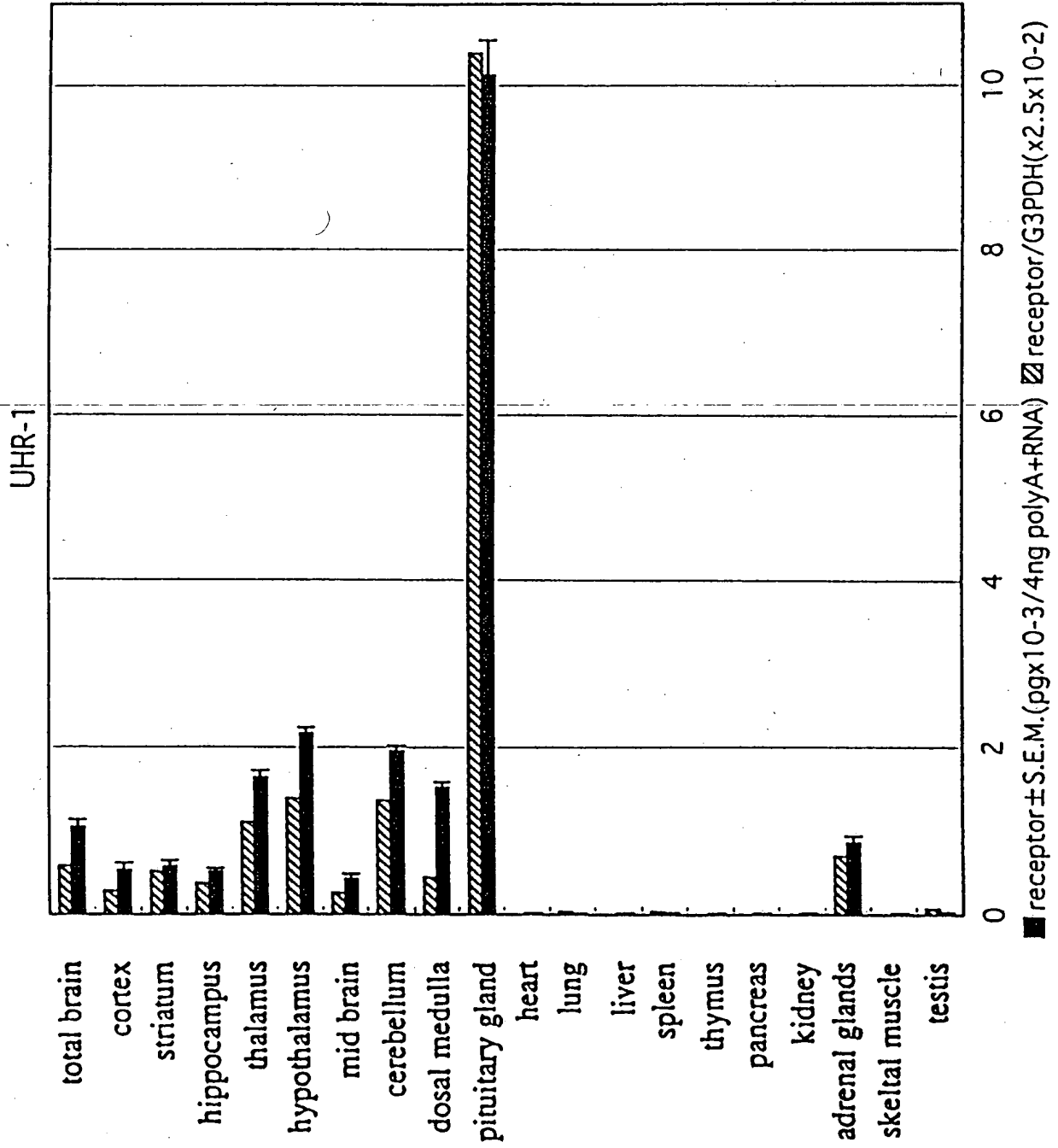


FIG. 38

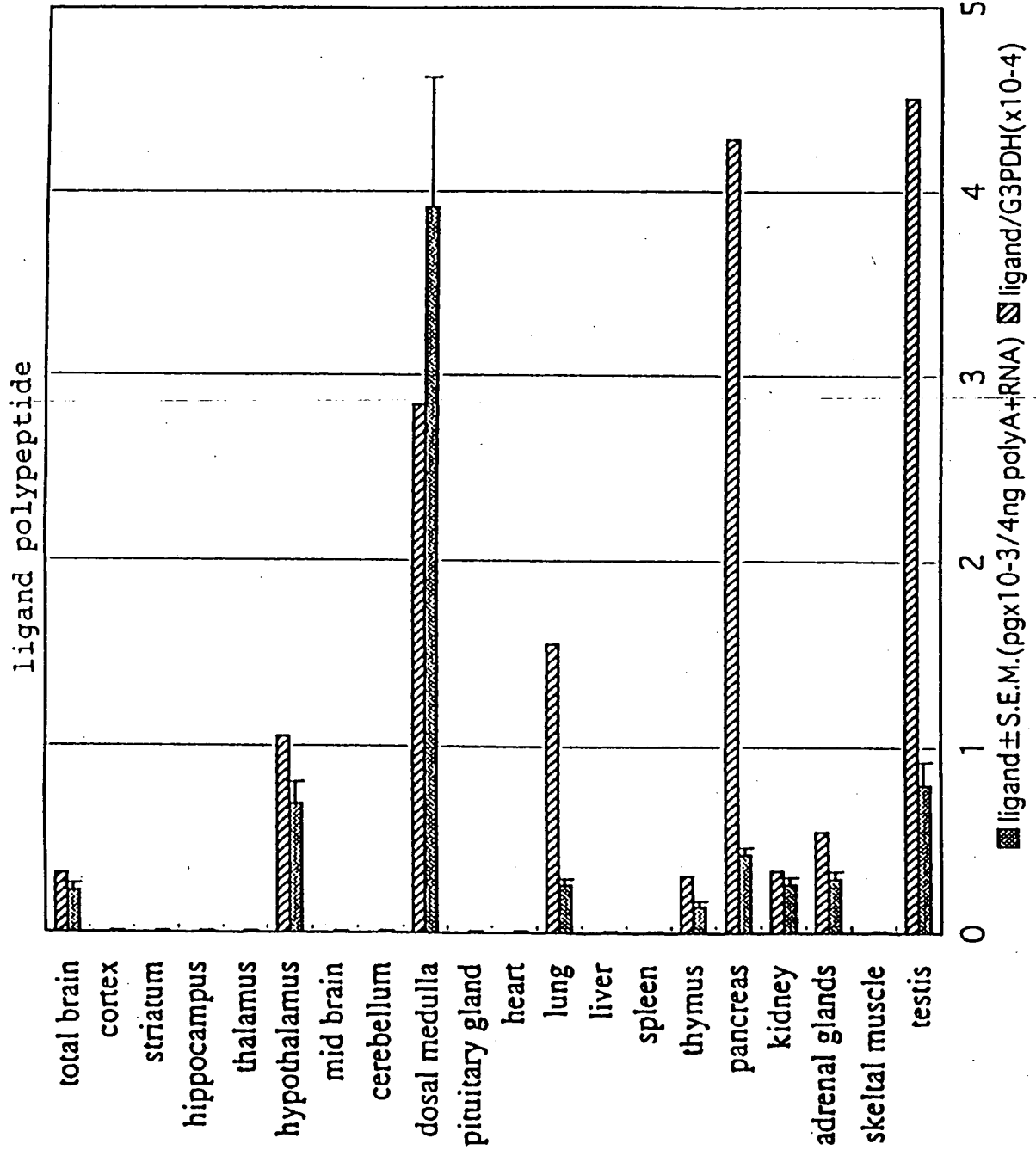


FIG. 39

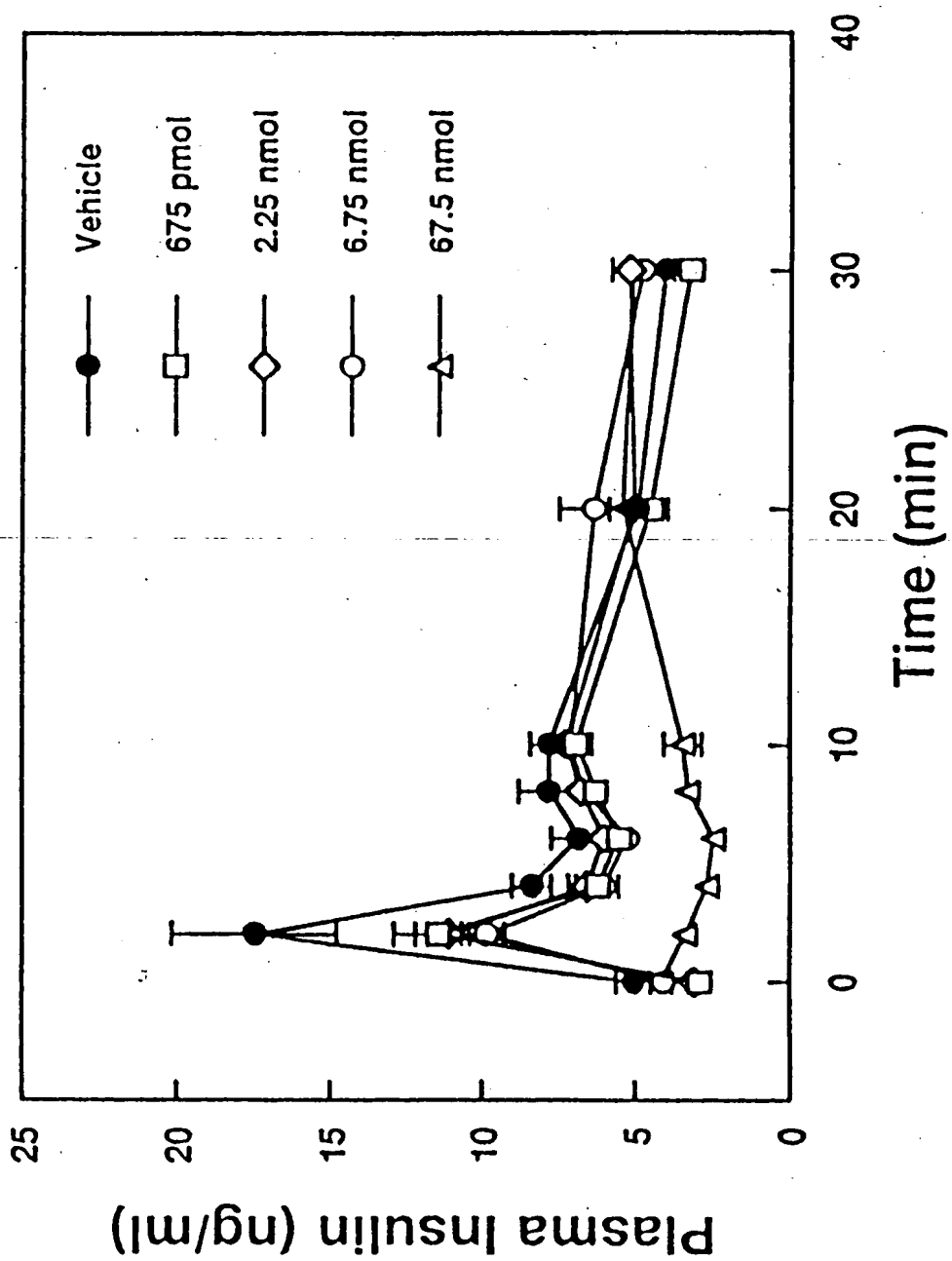


FIG. 40

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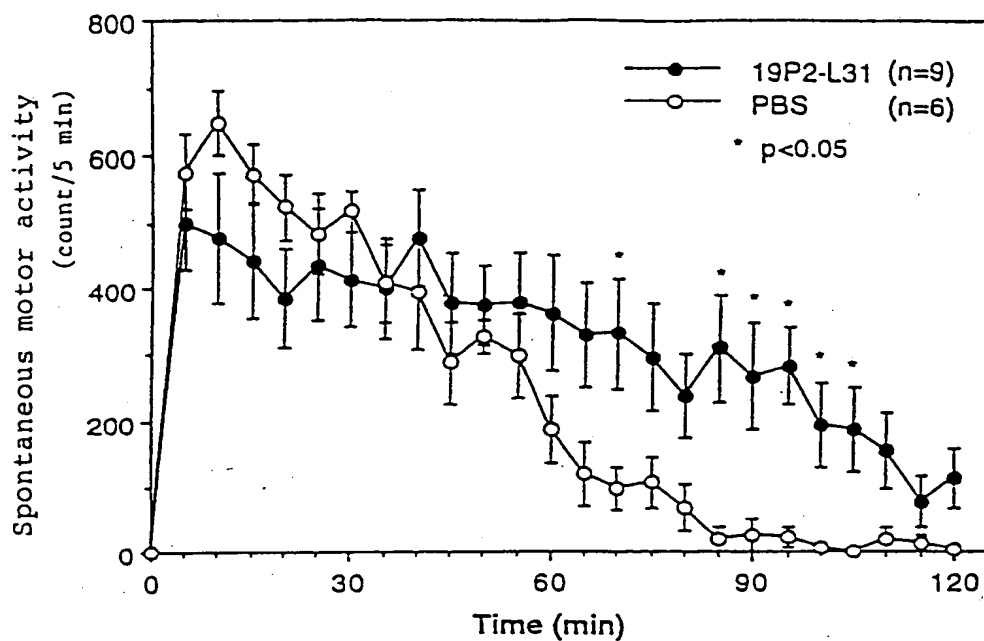


FIG. 41A

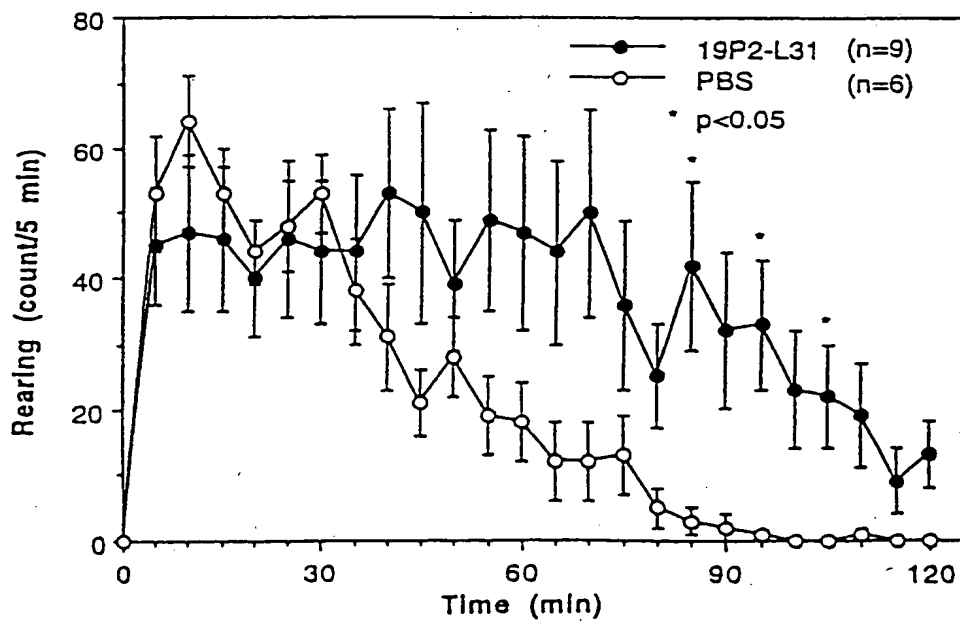


FIG. 41B

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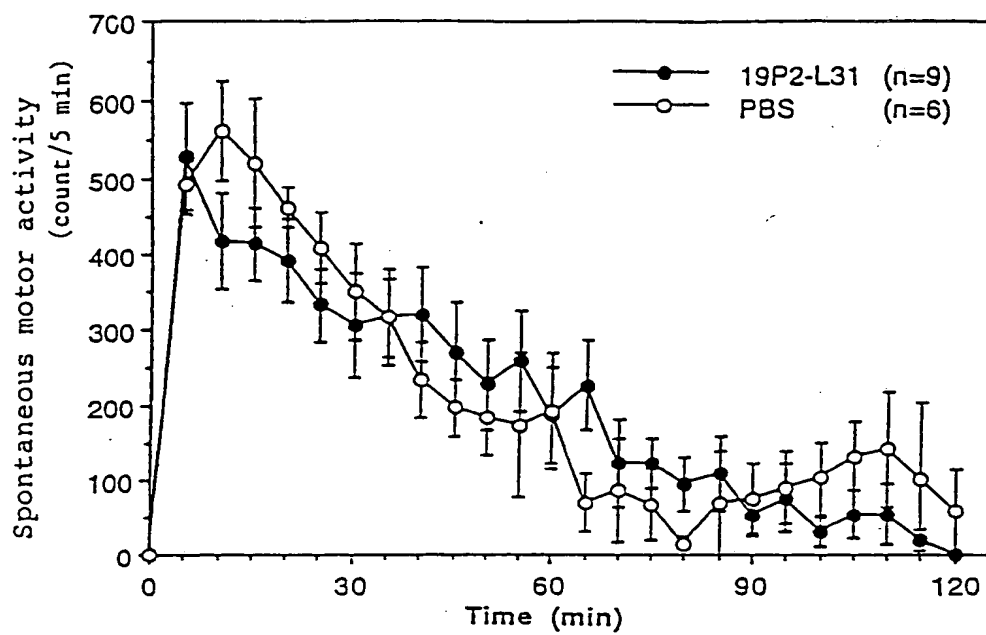


FIG. 42A

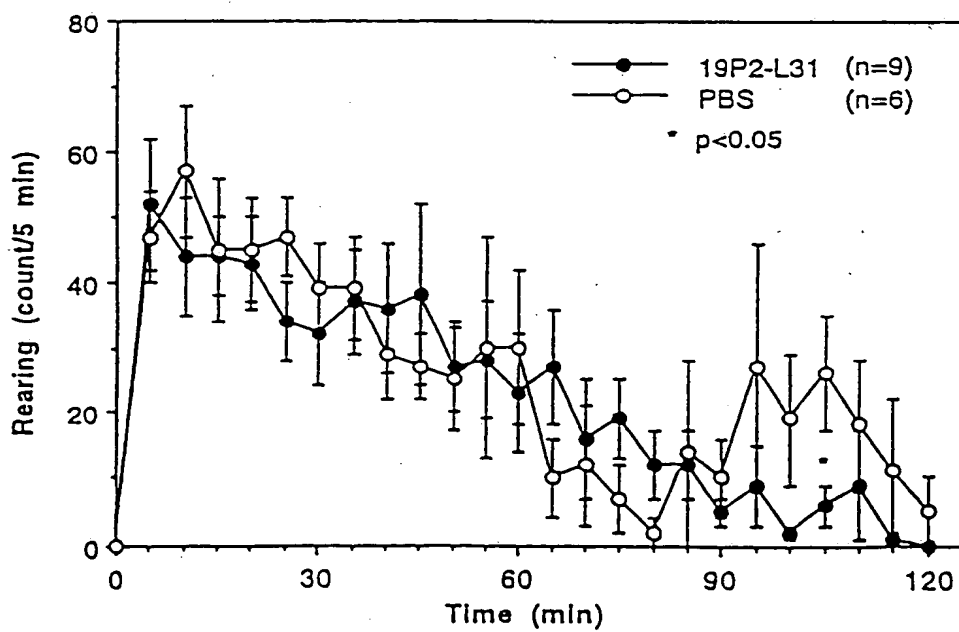


FIG. 42B

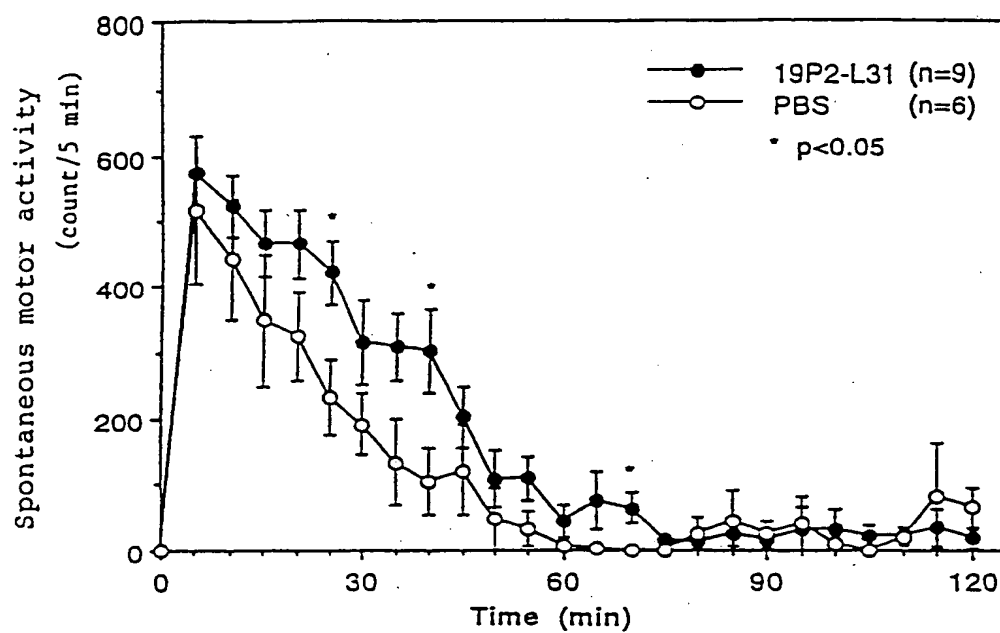


FIG. 43A

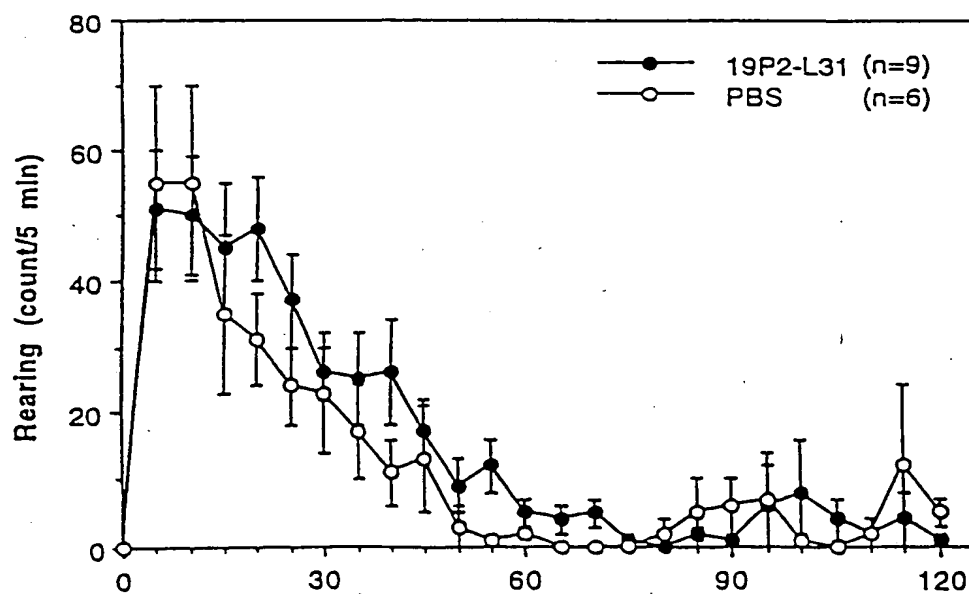


FIG. 43B

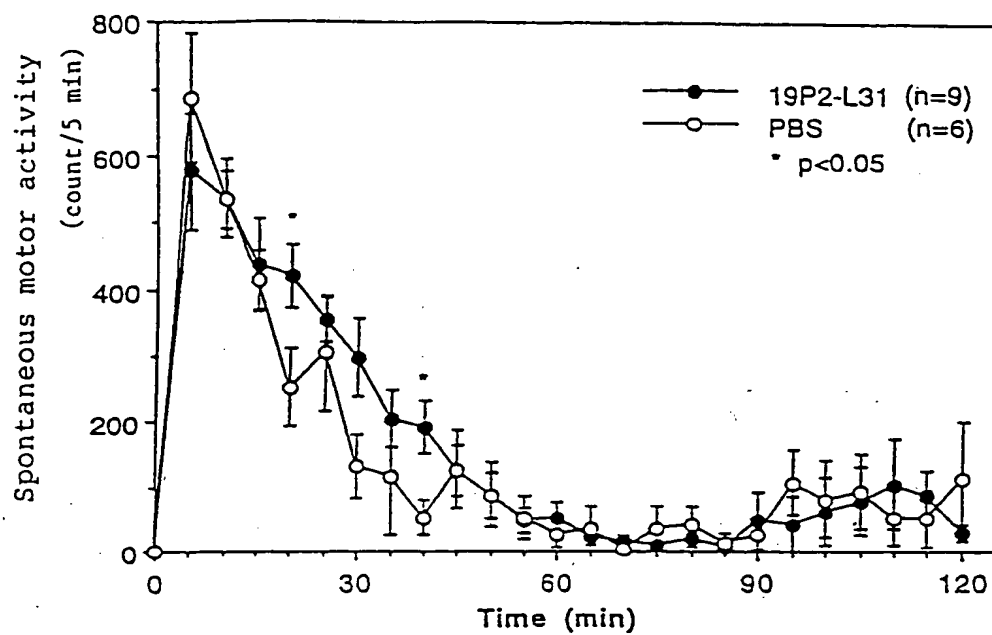


FIG. 44A

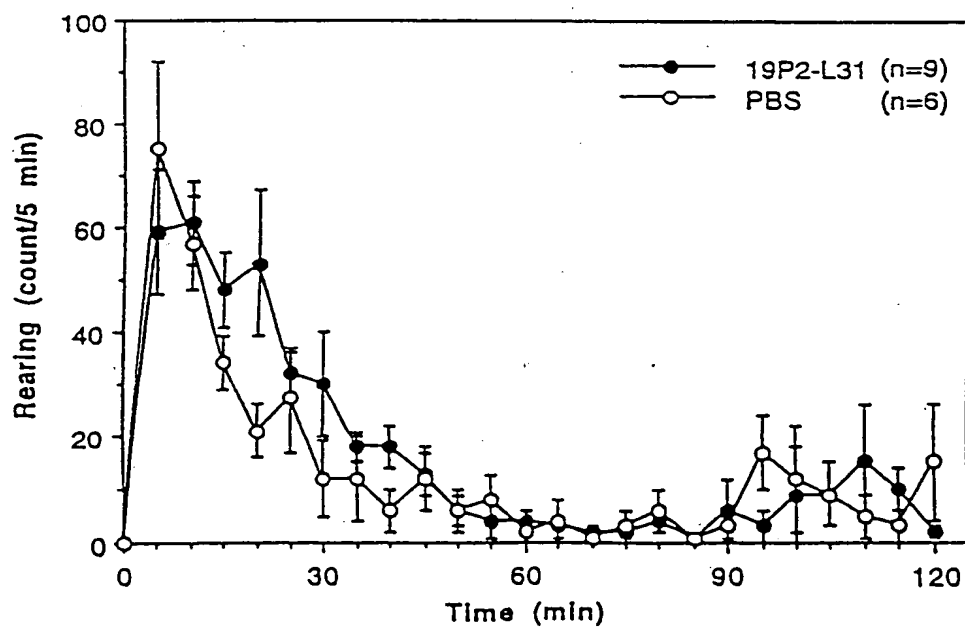


FIG. 44B

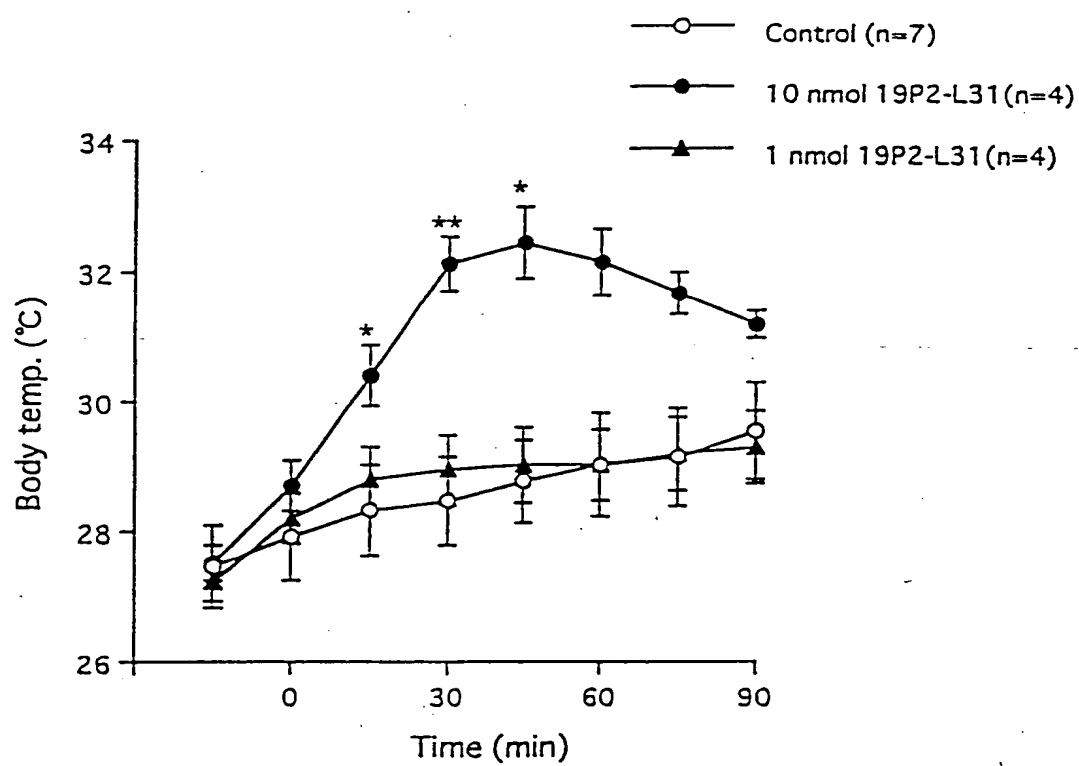


FIG. 45

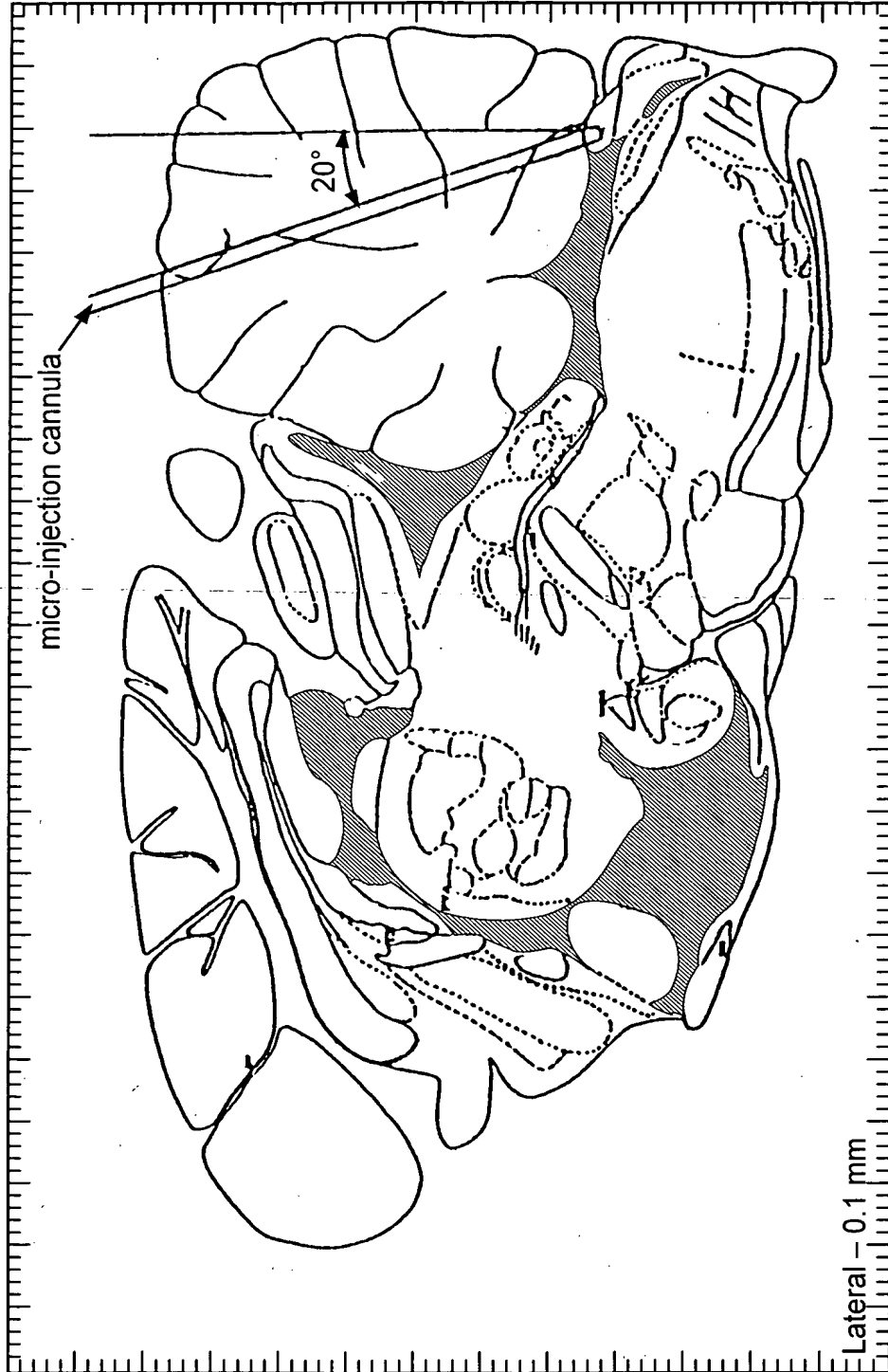


FIG. 46

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direct blood pressure

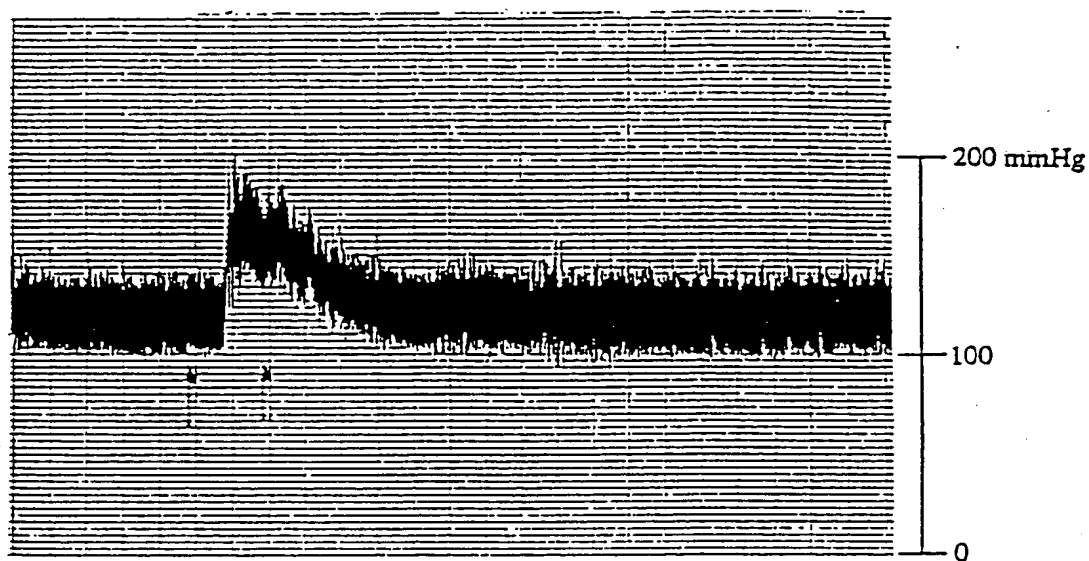


FIG. 47A

mean blood pressure

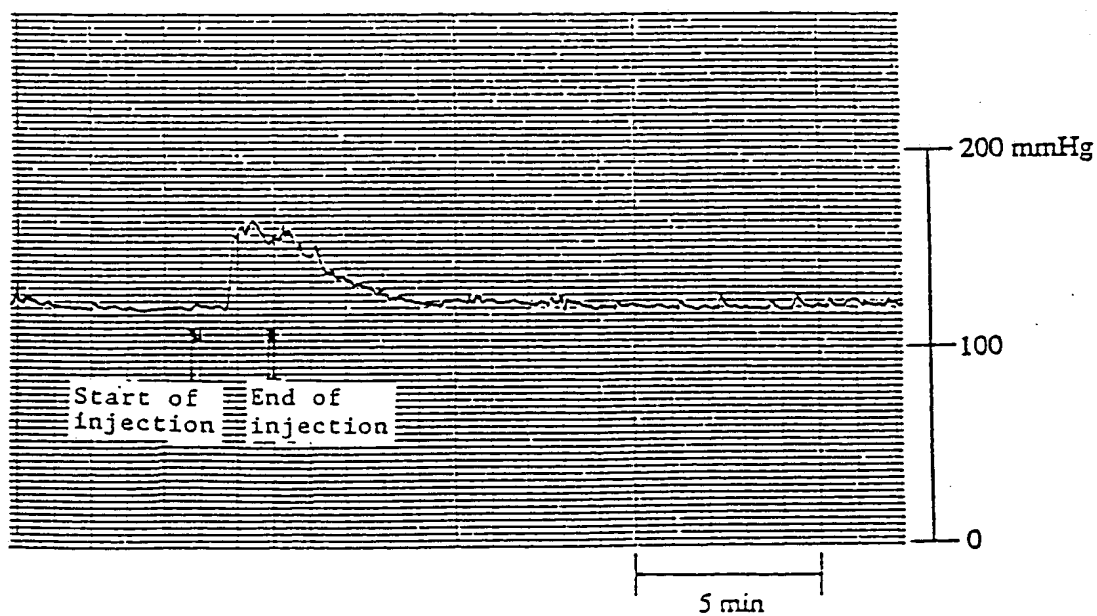


FIG. 47B

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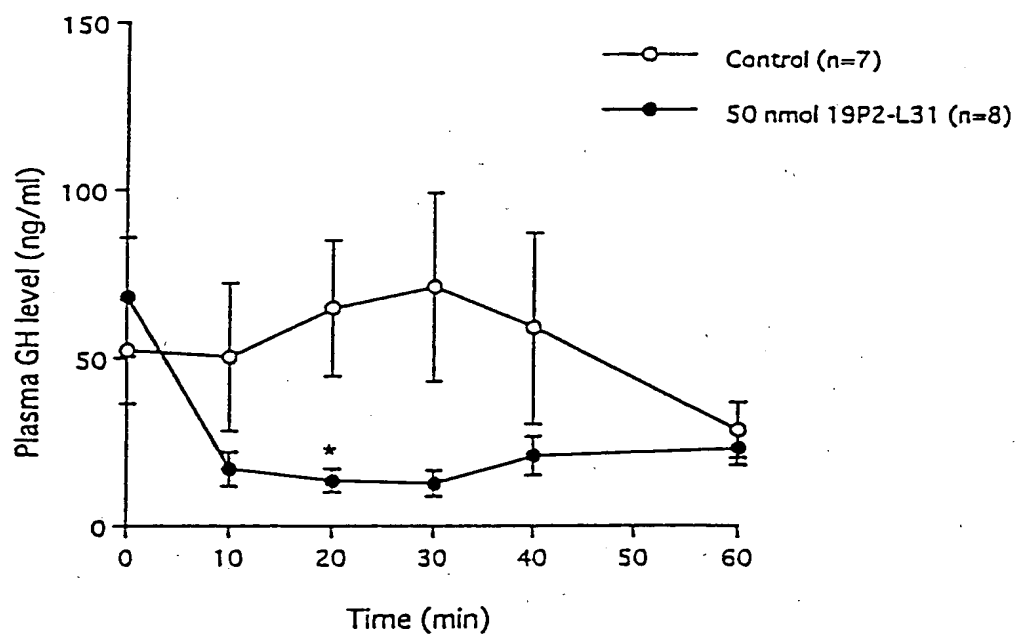


FIG. 48

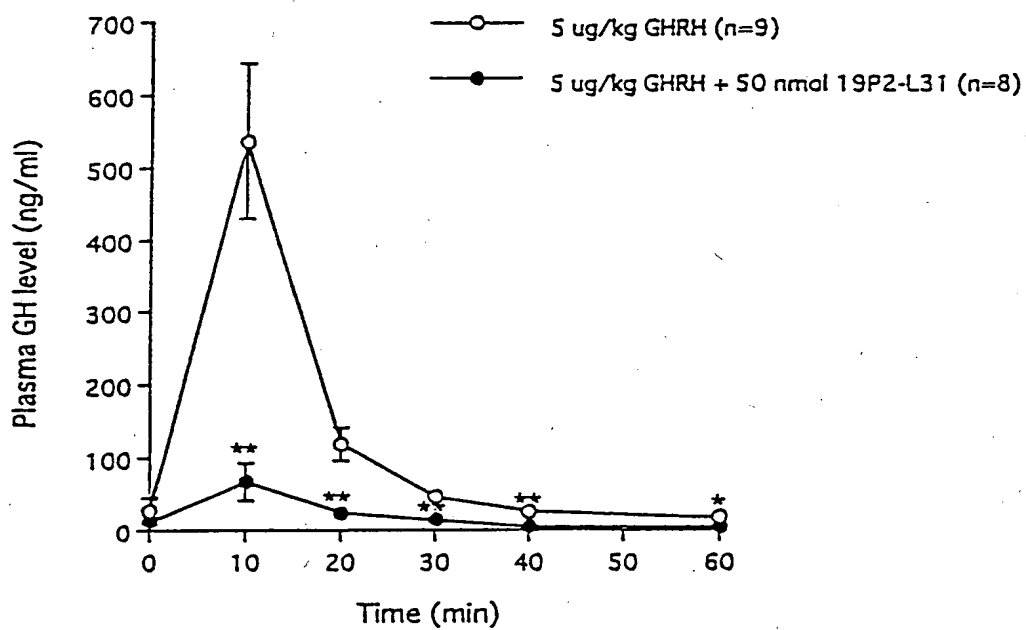


FIG. 49

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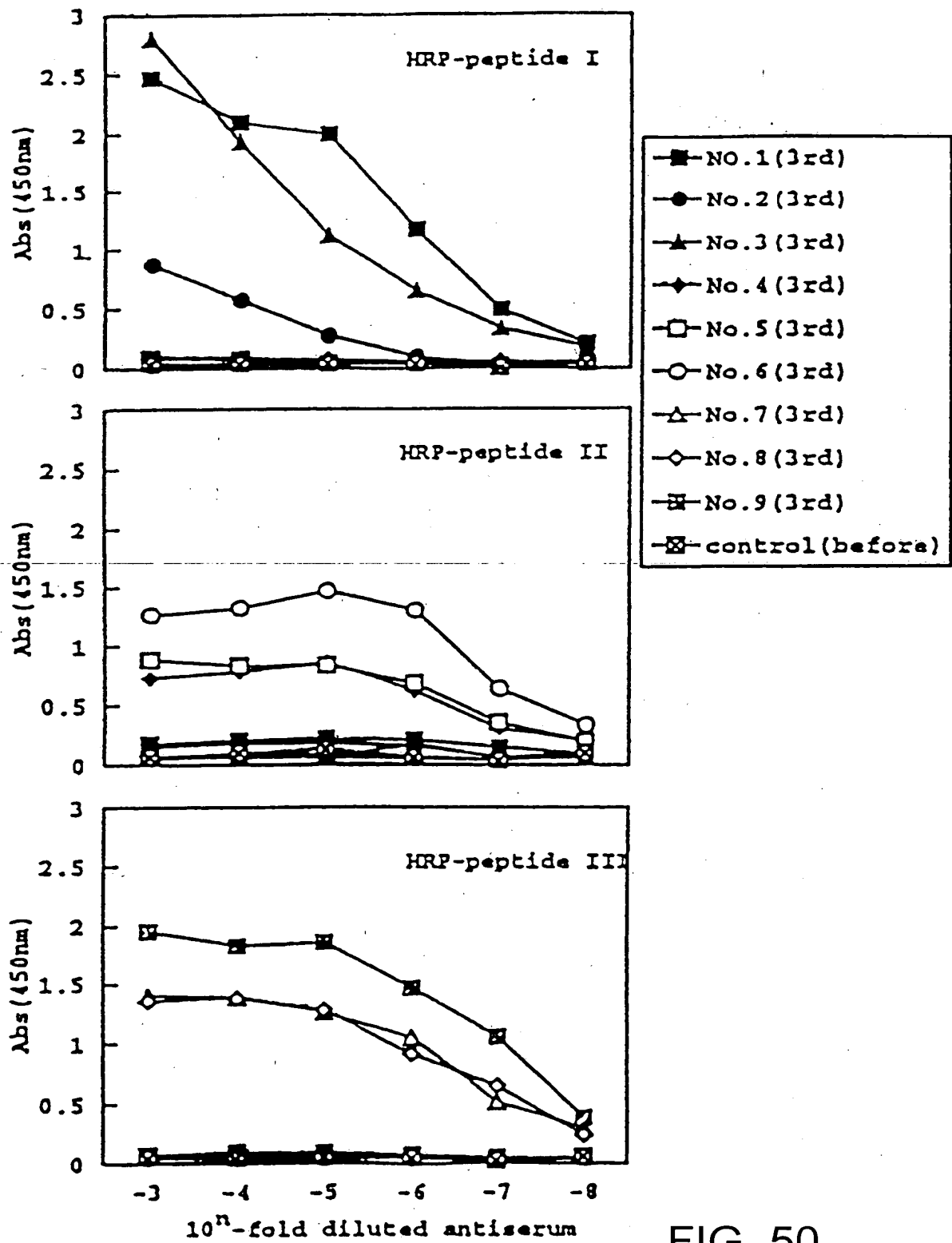


FIG. 50

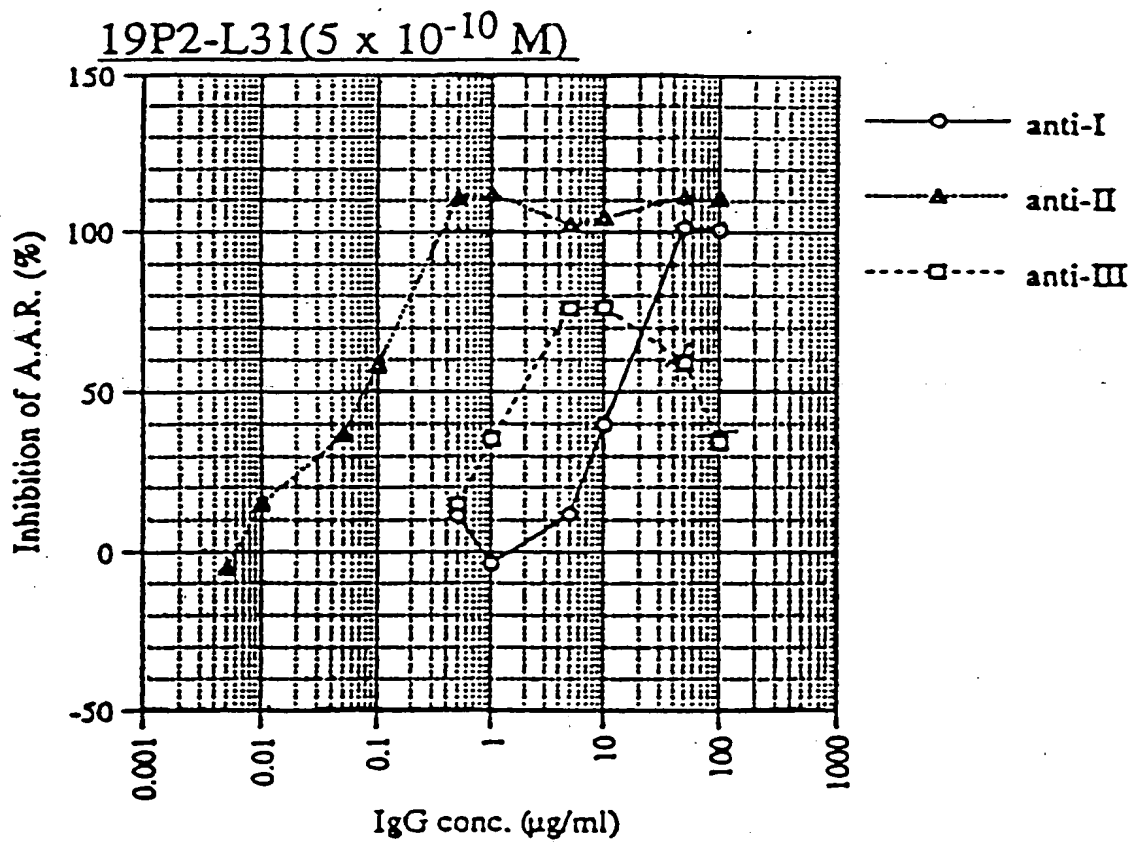


FIG. 51

FIG. 52A
FIG. 52B
FIG. 52C
FIG. 52D
FIG. 52E

FIG. 52A

FIG. 52

5'	9	18	27	36	45	54
ATG ACC TCA CTG CCC CCT GGA ACC ACT GGG GAC CCC GAT TTG TTT TCT GGG CCG						
Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser Gly Pro						
63	72	81	90	89	108	
TCG CCA GCC GGC TCC ACT CCA GCC AAC CAG AGT GCA GAG GCT TCA GAG AGC AAT						
Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser Glu Ser Asn						

117	126	135	144	153	162
GTG TCT GCG ACG GTT CCC AGA GCT GCA GCA GTC ACG CCG TTC CAG AGC CTG CAA					
Val Ser Ala Thr Val Pro Arg Ala Ala Val Thr Pro Phe Gln Ser Leu Gln					
171	180	189	198	207	216
CTA GTG CAC CAG CTG AAG GCA GCA CTG ATC GTG ATG CTG TAC AGC ATC GTG GTG GTC					
Leu Val His Gln Leu Lys Ala Leu Ile Val Met Leu Tyr Ser Ile Val Val Val					
225	234	243	252	261	270
GTG GGT CTG GTG GGC AAC TGC CTT CTT GTG CTG GTG ATC GCG GTG CGC CGG					
Val Gly Leu Val Gly Asn Cys Leu Leu Val Val Ile Ala Arg Val Arg Arg					
279	288	297	306	315	324
CTG CAC AAC GTG ACC AAC TTC CTC ATC GGC AAC CTG GCC TTT TCC GAT GTG CTC					
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu					
333	342	351	360	369	378
ATG TGT GCC GCC TGT GTG CCT CTC ACG CTG GCC TAC GCC TTT GAA CCT CGT GGC					
Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly					

FIG. 52B

387	TGG	GTG	TTC	GGT	GGA	GGC	CTG	TGC	CAC	CTT	GTT	TTC	414	CTG	CAG	CCG	GTG	ACC	432
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Trp	Val	Phe	Gly	Gly	Leu	Cys	His	Leu	Val	Phe	Phe	Leu	Gln	Pro	Val	Thr		
441	GTC	TAC	GTA	TCG	GTG	TTC	ACA	CTC	ACC	ACA	ATC	GCT	468	GAC	CGC	TAT	GTG	GTT	486
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Val	Tyr	Val	Ser	Val	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Val	Asp	Arg	Tyr	Val		
495	CTG	GTG	CAC	CCG	CTA	CGT	CGG	CGC	ATT	TCA	CTG	AAG	522	AGC	GCC	TAC	GTG	540	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Val	His	Pro	Leu	Arg	Arg	Ile	Ser	Leu	Lys	Leu	Ser	Ala	Tyr	Ala	Val		
549	CTG	GGC	ATC	TGG	GCT	CTA	TCT	GCA	GTG	CTG	GCG	CTG	576	GCC	GCG	GTG	CAC	594	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Leu	Gly	Ile	Trp	Ala	Leu	Ser	Ala	Val	Leu	Ala	Leu	Pro	Ala	Val	His	Thr		
603	TAC	CAT	GTA	GAG	CTC	AAG	CCC	CAC	GAC	GTG	CGC	CTC	630	GAG	GAG	TTC	TGG	648	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
	Tyr	His	Val	Glu	Leu	Lys	Pro	His	Asp	Val	Arg	Leu	Cys	Glu	Glu	Phe	Trp	Gly	

FIG. 52C

657	666	675	684	693	702
TCG CAG GAG CGC CAG CGA CAG ATC TAT GCC TGG GGG CTG CTG GGC ACC TAT					
---	---	---	---	---	---
Ser Gln Glu Arg Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Gly Thr Tyr					
711	720	729	738	747	756
TTG CTC CCC CTG CTG GCC ATT CTC CTG TCT TAC GTC CGG GTG TCG GTG AAG TTG					
---	---	---	---	---	---
Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu					
765	774	783	792	801	810
CGG AAC CGC GTG GTG CCT GGC AGC GTG ACC CAG AGC CAG GCT GAC TGG GAC CGA					
---	---	---	---	---	---
Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg					
819	828	837	846	855	864
GCG CGT CGC CGT CGC ACT TTC TGC CTG CTG CTG GTG GTG GTG TTC GCG					
---	---	---	---	---	---
Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala					
873	882	891	900	909	918
GTC TGC TGG CTG CCT CTG CAC ATT TTC AAC CTG CTG CGG GAC CTG GAC CCG CGT					
---	---	---	---	---	---
Val Cys Trp Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg					

FIG. 52D

927	936	945	954	963	972
GCC ATC GAC CCC TAC GCC TTC GGG CTG GTG CAG CTC CTC TGC CAC TGG CTT GCC					
Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys His Trp Leu Ala					
981	990	999	1008	1017	1026
ATG AGC TCC GCC TGC TAC AAC CCC TTC ATC ATC TAT GCG TCG CTG CAC GAC AGC TTC					
Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Ser Leu His Asp Ser Phe					
1035	1044	1053	1062	1071	1080
CGA GAG GAG CTA CGC AAG ATG CTT CTG TCT TGG CCC CGC AAG ATC GTG CCT CAT					
Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro His					
1089	1098	1107	1116		
GCC CAG AAT ATG ACC GTC AGT GTG GTC ATC TGA TGA					
Gly Gln Asn Met Thr Val Ser Val Val Ile					

1'

FIG. 52E

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